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(54) Title: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS OF USE

(57) Abstract

The complete sequence of the canine von Willebrand Factor cDNA and deduced amino acid sequence is provided. The mutation which causes von Willebrand's Disease in Scottish Terriers, a single base deletion in exon 4, has also been determined. Methods for detecting carriers of the defective vWF gene are also provided.

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DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS OF USE

FIELD OF THE INVENTION

This invention relates generally to canine von Willebrand factor (vWF), and more particularly, to the gene encoding vWF as well as a genetic defect that causes canine von Willebrand's disease.

BIOLOGICAL DEPOSITS

SEQUENCE	ACCESSION NO.
Canine von Willebrand Factor	

BACKGROUND OF THE INVENTION

In both dogs and humans, von Willebrand's disease (vWD) is a bleeding disorder of variable severity that results from a quantitative or qualitative defect in von Willebrand factor (vWF) (Ginsburg, D. et al., *Blood* 79:2507-2519 (1992); Ruggeri, Z.M., et al., *FASEB J* 7:308-316 (1993); Dodds, W.J., *Mod Vet Pract* 681-686 (1984); Johnson, G.S. et al., *JAVMA* 176:1261-1263 (1988); Brooks, M., *Probl In Vet Med* 4:636-646 (1992)). This clotting factor has two known functions, stabilization of Factor VIII (hemophilic factor A) in the blood, and aiding the adhesion of platelets to the subendothelium, which allows them to provide hemostasis more effectively. If the factor is missing or defective, the patient, whether human or dog, may bleed severely.

The disease is the most common hereditary bleeding disorder in both species, and is genetically and clinically heterogenous. Three clinical types, called 1, 2, and 3 (formerly I, II, and III; see Sadler, J.E. et al., *Blood* 84:676-679 (1994) for nomenclature changes), have been described. Type 1 vWD is inherited in a dominant, incompletely penetrant fashion. Bleeding appears to be due to the reduced level of vWF rather than a qualitative difference. Although this is the most common form of vWD found in most mammals, and can cause serious bleeding problems, it is generally less severe than the other two types. In addition, a relatively inexpensive vasopressin analog (DDAVP) can help alleviate symptoms (Kraus, K.H. et al., *Vet Surg* 18:103-109 (1989)).

In Type 2 vWD, patients have essentially normal levels of vWF, but the factor is abnormal as determined by specialized tests (Ruggeri, Z.M., et al., *FASEB J* 7:308-316 (1993); Brooks, M., *Probl In Vet Med* 4:636-646 (1992)). This type is also

inherited in a dominant fashion and has only rarely been described in dogs (Turrentine, M.A., et al., *Vet Clin North Am Small Anim Pract* 18:275 (1988)).

Type 3 vWD is the most severe form of the disease. It is inherited as an autosomal recessive trait, and affected individuals have no detectable vWF in their blood. Serious bleeding episodes require transfusions of blood or cryoprecipitate to supply the missing vWF. Heterozygous carriers have moderately reduced factor concentrations, but generally appear to have normal hemostasis.

Scottish terriers have Type 3 vWD (Dodds, W.J., *Mod Vet Pract* 681-686 (1984); Johnson, G.S. et al., *JAVMA* 176:1261-1263 (1988)). Homozygotes have no detectable vWF and have a severe bleeding disorder. Heterozygotes have reduced levels of the factor, and are clinically normal (Brooks, M. et al., *JAVMA* 200:1123-1127 (1992)). The prevalence of vWD among Scottish terriers including both heterozygotes and homozygotes has been variously estimated from 27-31% (Stokol, T. et al., *Res. Vet. Sci.* 59:152-155 (1995); Brooks, M., *Proc. 9th ACVIM Forum* 89-91 (1991)).

Currently, detection of affected and carrier Scottish terrier dogs is done by vWF antigen testing (Benson, R.E. et al., *Am J Vet Res* 44:399-403 (1983); Stokol, T. et al., *Res. Vet. Sci.* 59:152-155 (1995)) or by coagulation assays (Rosborough, T.K. et al., *J. Lab. Clin. Med.* 96:47-56 (1980); Read, M.S. et al., *J. Lab. Clin. Med.* 101:74-82 (1983)). These procedures yield variable results, as the protein-based tests can be influenced by such things as sample collection, sample handling, estrous, pregnancy, vaccination, age, and hypothyroidism (Strauss, H.S. et al., *New Eng J Med* 269:1251-1252 (1963); Bloom, A.L., *Mayo Clin Proc* 66:743-751 (1991); Stirling, Y. et al., *Thromb Haemostasis* 52:176-182 (1984); Mansell, P.D. et al., *Br. Vet. J.* 148:329-337 (1992); Avgeris, S. et al., *JAVMA* 196:921-924 (1990); Panciera, D.P. et al., *JAVMA* 205:1550-1553 (1994)). Thus, for example, a dog that tests within the normal range on one day, can test within the carrier range on another day. It is therefore difficult for breeders to use this information.

It would thus be desirable to provide the nucleic acid sequence encoding canine vWF. It would also be desirable to provide the genetic defect responsible for canine vWD. It would further be desirable to obtain the amino acid sequence of canine vWF. It would also be desirable to provide a method for detecting carriers of the defective vWF gene based on the nucleic acid sequence of the normal and defective vWF gene.

SUMMARY OF THE INVENTION

The present invention provides a novel purified and isolated nucleic acid sequence encoding canine vWF. A nucleic acid sequence containing the mutation that causes vWD in Scottish terriers, a single-base deletion in exon 4, is also provided. The nucleic acid sequences of the present invention may be used in methods for detecting carriers of the mutation that causes vWD. Such methods may be used by breeders to reduce the frequency of the disease-causing allele and the incidence of disease. In addition, the nucleic acid sequence of the canine vWF provided herein may be used to determine the genetic defect that causes vWD in other breeds as well as other species.

Additional objects, advantages, and features of the present invention will become apparent from the following description, taken in conjunction with the accompanying drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

The various advantages of the present invention will become apparent to one skilled in the art by reading the following specification and by referencing the following drawings in which:

Figures 1A-1C is the nucleic acid sequence of the canine von Willebrand factor of the present invention;

Figures 2A-2C is a comparison of the human and canine prepro-von Willebrand factor amino acid sequences;

Figure 3 provides nucleotide sequencing ladders for the von Willebrand's disease mutation region for normal (clear), carrier, and affected Scottish terriers, the sequences being obtained directly from PCR products derived from genomic DNAs in exon 4;

Figure 4 illustrates the results of a method of the present invention used to detect the Scottish terrier vWD mutation; and

Figure 5 shows the Scottish terrier pedigree, which in turn illustrates segregation of the mutant and normal vWF alleles.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The cDNA encoding canine von Willebrand Factor (vWF) has been sequenced, and its sequence is set forth in Figures 1A-1C and SEQ ID NO: 1. The amino acid sequence corresponding to the cDNA of canine vWF has been subsequently deduced and is set forth in Figures 2A-2C and SEQ ID NO: 2. The mutation of the normal vWF gene which causes von Willebrand's Disease (vWD),

a deletion at codon 88 of the normal gene resulting in a frameshift, is also provided. The nucleic acid sequences of the present invention may be used in methods for detecting homozygous and heterozygous carriers of the defective vWF gene.

In a preferred method of detecting the presence of the von Willebrand allele in canines, DNA samples are first collected by relatively noninvasive techniques, *i.e.*, DNA samples are obtained with minimal penetration into body tissues of the animals to be tested. Common noninvasive tissue sample collection methods may be used and include withdrawing buccal cells via cheek swabs and withdrawing blood samples. Following isolation of the DNA by standard techniques, PCR is performed on the DNA utilizing pre-designed primers that produce enzyme restriction sites on those DNA samples that harbor the defective gene. Treatment of the amplified DNA with appropriate restriction enzymes such as *Bsi*E I thus allows one to analyze for the presence of the defective allele. One skilled in the art will appreciate that this method may be applied not only to Scottish terriers, but to other breeds such as Shetland sheepdogs and Dutch Kooikers.

Overall, the present invention provides breeders with an accurate, definitive test whereby the undesired vWD gene may be eliminated from breeding lines. The current tests used by breeders are protein- based, and as noted previously, the primary difficulty with this type of test is the variability of results due to a variety of factors. The ultimate result of such variability is that an inordinate number of animals fall into an ambiguous grouping whereby carriers and noncarriers cannot be reliably distinguished. The present invention obviates the inherent limitations of protein-based tests by detecting the genetic mutation which causes vWD. As described in Specific Example 1, the methods of the present invention provide an accurate test for distinguishing noncarriers, homozygous carriers and heterozygous carriers of the defective vWF gene.

It will be appreciated that because the vWF cDNA of the present invention is substantially homologous to vWF cDNA throughout the canine species, the nucleic acid sequences of the present invention may be used to detect DNA mutations in other breeds as well. In addition, the canine vWF sequence presented herein potentially in combination with the established human sequence (Genbank Accession No. X04385, Bonthron, D. et al., *Nucleic Acids Res.* 14:7125-7128 (1986); Mancuso, D.J. et al., *Biochemistry* 30:253-269 (1989); Meyer, D. et al., *Throm Haemostasis* 70:99-104 (1993)), may be used to facilitate sequencing of the vWF

gene and genetic defects causing vWD, in other mammalian species *e.g.*, by using cross-species PCR methods known by those skilled in the art.

It is also within the contemplation of this invention that the isolated and purified nucleic acid sequences of the present invention be incorporated into an appropriate recombinant expression vector, *e.g.*, viral or plasmid, which is capable of transforming an appropriate host cell, either eukaryotic (*e.g.*, mammalian) or prokaryotic (*e.g.*, *E. coli*). Such DNA may involve alternate nucleic acid forms, such as cDNA, gDNA, and DNA prepared by partial or total chemical synthesis. The DNA may also be accompanied by additional regulatory elements, such as promoters, operators and regulators, which are necessary and/or may enhance the expression of the vWF gene product. In this way, cells may be induced to over-express the vWF gene, thereby generating desired amounts of the target vWF protein. It is further contemplated that the canine vWF polypeptide sequence of the present invention may be utilized to manufacture canine vWF using standard synthetic methods. One skilled in the art will also note that the defective protein encoded by the defective vWF gene of the present invention may also be of use in formulating a complementary diagnostic test for canine vWD that may provide further data in establishing the presence of the defective allele. Thus, production of the defective vWF polypeptide, either through expression in transformed host cells as described above for the active vWF polypeptide or through chemical synthesis, is also contemplated by the present invention.

The term "gene" as to referred herein means a nucleic acid which encodes a protein product. The term "nucleic acid" refers to a linear array of nucleotides and nucleosides, such as genomic DNA, cDNA and DNA prepared by partial or total chemical synthesis from nucleotides. The term "encoding" means that the nucleic acid may be transcribed and translated into the desired polypeptide. "Polypeptide" refers to amino acid sequences which comprise both full-length proteins and fragments thereof. "Mutation" as referred to herein includes any alteration in a nucleic acid sequence including, but not limited to, deletions, substitutions and additions.

As referred to herein, the term "capable of hybridizing under high stringency conditions" means annealing a strand of DNA complementary to the DNA of interest under highly stringent conditions. Likewise, "capable of hybridizing under low stringency conditions" refers to annealing a strand of DNA complementary to the DNA of interest under low stringency conditions. In the present invention, hybridizing

under either high or low stringency conditions would involve hybridizing a nucleic acid sequence (*e.g.*, the complementary sequence to SEQ ID NO: 1 or portion thereof), with a second target nucleic acid sequence. "High stringency conditions" for the annealing process may involve, for example, high temperature and/or low salt content, which disfavor hydrogen bonding contacts among mismatched base pairs. "Low stringency conditions" would involve lower temperature, and/or lower salt concentration than that of high stringency conditions. Such conditions allow for two DNA strands to anneal if substantial, though not near complete complementarity exists between the two strands, as is the case among DNA strands that code for the same protein but differ in sequence due to the degeneracy of the genetic code. Appropriate stringency conditions which promote DNA hybridization, for example, 6X SSC at about 45 °C, followed by a wash of 2X SSC at 50 °C are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (1989), 6.31-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2X SSC at 50 °C to a high stringency of about 0.2X SSC at 50 °C. In addition, the temperature in the wash step can be increased from low stringency at room temperature, about 22 °C, to high stringency conditions, at about 65 °C. Other stringency parameters are described in Maniatis, T., et al., *Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press*, Cold Spring NY, (1982), at pp. 387-389; see also Sambrook J. et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Volume 2, Cold Spring Harbor Laboratory Press, Cold Spring, NY at pp. 8.46-8.47 (1989).

SPECIFIC EXAMPLE 1

Materials And Methods

Isolation of RNA. The source of the RNA was a uterus from a Scottish Terrier affected with vWD (factor level < 0.1% and a clinical bleeder), that was surgically removed because of infection. Spleen tissue was obtained from a Doberman Pinscher affected with vWD that died from dilated cardiomyopathy (factor level 7% and a clinical bleeder). Total RNA was extracted from the tissues using Trizol (Life Technologies, Gaithersburg, MD). The integrity of the RNA was assessed by agarose gel electrophoresis.

Design of PCR primer sets. Primers were designed to a few regions of the gene, where sequences from two species were available (Lavergne, J.M. et al., *Biochem Biophys Res Commun* 194:1019-1024 (1993); Bakhshi, M.R. et al., *Biochem Biophys Acta* 1132:325-328 (1992)). These primers were designed using

rules for cross-species' amplifications (Venta et al., "Genes-Specific Universal Mammalian Sequence-Tagged Sites: Application To The Canine Genome" *Biochem. Genet.* (1996) in press). Most of the primers had to be designed to other regions of the gene using the human sequence alone (Mancuso, D.J. et al., *Biochemistry* 30:253-269 (1991)). Good amplification conditions were determined by using human and canine genomic DNAs.

Reverse Transcriptase-PCR. Total RNA was reverse transcribed using random primers (Bergenhem, N.C.H. et al., *PNAS (USA)* 89:8789-8802 (1992)). The cDNA was amplified using the primer sets shown to work on canine genomic DNA.

DNA Sequence Analysis. Amplification products of the predicted sizes were isolated from agarose gels by adsorption onto silica gel particles using the manufacturer's method (Qiagen, Chatsworth, CA). Sequences were determined using ^{32}P-5′ end-labeled primers and a cycle sequencing kit (United States Biochemical Corp., Cleveland, OH). The sequences of the 5′ and 3′ untranslated regions were determined after amplification using Marathon™ RACE kits (Clontech, Palo Alto, CA). Sequences were aligned using the Eugene software analysis package (Lark Technologies, Houston, TX). The sequence of the canine intron four was determined from PCR-amplified genomic DNA.

Design of a Diagnostic Test. PCR mutagenesis was used to create diagnostic and control *Bsi*E I and *Sau*96 I restriction enzyme sites for the test. Amplification conditions for the test are: 94°C, 1 min, 61°C, 1 min, and 72°C, 1 min, for 50 cycles using cheek swab DNA (Richards, B. et al., *Human Molecular Genetics* 2:159-163 (1992)).

Population Survey. DNA was collected from 87 Scottish terriers from 16 pedigrees. DNA was isolated either from blood using standard procedures (Sambrook, J. et al., Cold Harbor Spring Lab, Cold Harbor Spring NY, 2nd Edition, (1989)) or by cheek swab samples (Richards, B. et al., *Human Molecular Genetics* 2:159-163 (1992)). The genetic status of each animal in the survey was determined using the *Bsi*E I test described above.

Results

Comparison of the canine and human sequences. The alignment of the canine and human prepro-von Willebrand Factor amino acid sequences is shown in Figures 2A-2C. The location of the Scottish terrier vWD mutation is indicated by the "*". Potential N-glycosylation sites are shown in bold type. The known and postulated integrin binding sites are boxed. Amino acid numbers are shown on the

right side of the figure. The human sequence is derived from Genbank accession number X04385 (Bonthron, D. et al., *Nucleic Acids Res.* 14:7125-7128 (1986)).

Overall, 85.1% sequence identity is seen between the prepro-vWF sequences. The pro-region is slightly less conserved than the mature protein (81.4% vs. 87.5%). There were no other noteworthy percentage sequence identity differences seen in other regions of the gene, or between the known repeats contained within the gene (data not shown). Fourteen potential N-linked glycosylation sites are present in the canine sequence, all of which correspond to similar sites contained within the human sequence. The two integrin binding sites identified in the human vWF protein sequence (Lankhof, H. et al., *Blood* 86:1035-1042 (1995)) are conserved in the canine sequence as well (Figures 2A-2C). The 5′ and 3′ untranslated regions have diverged to a greater extent than the coding region (data not shown), comparable to that found between the human and bovine sequences derived for the 5′ flanking region (Janel, N. et al., *Gene* 167:291-295 (1995)). Additional insights into the structure and function of the von Willebrand factor can be gained by comparison of the complete human sequence (Mancuso, D.J. et al., *Biochemistry* 30:253-269 (1989); Meyer, D. et al., *Throm Haemostasis* 70:99-104 (1993)) and the complete canine sequence reported here.

The sequence for most of exon 28 was determined (Mancuso, D.J. et al., *Thromb Haemost* 69:980 (1993); Porter, C.A. et al., *Mol Phylogenet Evol* 5:89-101 (1996)). All three sequences are in complete agreement, although two silent variants have been found in other breeds (Table 1, exon 28). Partial sequences of exons 40 and 41 (cDNA nucleotide numbers 6923 to 7155, from the initiation codon) were also determined as part of the development of a polymorphic simple tandem repeat genetic marker (Shibuya, H. et al., *Anim Genet* 24:122 (1994)). There is a single nucleotide sequence difference between this sequence ("T") and the sequence of the present invention, ("C") at nucleotide position 6928.

Scottish Terrier vWD mutation. Figure 3 shows nucleotide sequencing ladders for the von Willebrand's Disease mutation region for normal (clear), carrier, and affected Scottish terriers. The sequences were obtained directly from PCR products derived from genomic DNAs in exon 4. The arrowheads show the location of the C nucleotide that is deleted in the disease-causing allele. Note that in the carrier ladder each base above the point of the mutation has a doublet appearance, as predicted for deletion mutations. The factor levels reported for these animals were: Normal, 54%; Carrier, 34%; Affected, <0.1%.

As a result of the deletion, a frameshift mutation at codon 88 leads to a new stop codon 103 bases downstream. The resulting severely truncated protein of 119 amino acids does not include any of the mature von Willebrand factor region. The identity of the base in the normal allele was determined from an unaffected dog.

Development of a diagnostic test. A PCR primer was designed to produce a *BsiE* I site in the mutant allele but not in the normal allele (Figure 4). The position of the deleted nucleotide is indicated by an asterisk. The altered nucleotides in each primer are underlined. The normal and mutant allele can also be distinguished using *Sau*96 I. The naturally occurring *Sau*96 I sites are shown by double underlines. The highly conserved donor and acceptor dinucleotide splice sequences are shown in bold type.

In order to ensure that the restriction enzyme cut the amplified DNA to completion, an internal control restriction site common to both alleles was designed into the non-diagnostic primer. The test was verified by digestion of the DNA from animals that were affected, obligate carriers, or normal (based on high factor levels [greater than 100% of normal] obtained from commonly used testing labs and reported to us by the owners, and also using breeds in which Type 3 vWD has not been observed). The expected results were obtained (*e.g.*, Figure 5). Five vWD-affected animals from a colony founded from Scottish terriers (Brinkhous, K.M. et al., *Ann. New York Acad. Sci.* 370:191-203 (1981)) were also shown to be homozygous for this mutation. An additional unaffected animal from this same colony was found to be clear.

It would still be possible to misinterpret the results of the test if restriction enzyme digestion was not complete, and if the rates of cleavage of the cont778rol and diagnostic sites were vastly different. The rates of cleavage of the two *BsiE* I sites were thus examined by partially digesting the PCR products and running them on capillary electrophoresis. The rates were found to be very nearly equal (the diagnostic site is cut 12% faster than the control site).

The mutagenesis primer was also designed to produce a *Sau*96 I site into the normal allele but not the mutant allele. This is the reverse relationship compared to the *BsiE* I-dependent test, with respect to which allele is cut. Natural internal *Sau*96 I sites serve as digestion control sites (shown in Figure 4). The test using this enzyme produced identical genotypic results compared to the *BsiE* I for all animals examined (data not shown).

A possible mutation in the Doberman Pinscher gene. The complete Scottish terrier sequence was compared to the complete Doberman Pinscher sequence. Several nucleotide differences were found and were compared to the nucleotides found in the same position in the human sequence as shown in Table 1 below. Most of these changes were silent. However, of three amino acid changes, one is relatively non-conservative (F905L) and is proposed to be the mutation that causes Doberman Pinscher vWD. Other data strongly suggest that the nucleotide interchange at the end of exon 43 causes a cryptic splice site to be activated reducing the amount of normally processed mRNA, with a concomitant decrease in the amount of vWF produced.

Mendelian inheritance. One test often used to verify the correct identification of a mutant allele is its inheritance according to Mendel's law of segregation. Three pedigrees were examined in which the normal and mutant alleles were segregating, as shown in Figure 5. Exon four of the vWF gene was PCR-amplified from genomic DNA. The PCR products were examined for the presence of the normal and mutant vWF alleles by agarose gel electrophoresis after digestion with *Bsi*E I (see Figure 5). The affected animals are homozygous for the mutant allele (229 bp; lanes 3 and 5). The other animals in this pedigree are heterozygotes (251 bp and 229 bp; lanes 1, 2, 4, and 6), including the obligate carrier parents.

Table 1 - Differences Between Scottie And Doberman Protein And Nucleotide von Willebrand Factor Sequences With Comparison To The Human Sequences

		Amino Acid			Codon		
Exon	A.A.[1]	Human	Scottie	Doberman	Human	Scottie	Doberman
5' UT[2]	nuc - 35[3]	N/A[4]	N/A	N/A	N/A	A	G
4	85	S	S/F.Shift[5]	S	TCC	TCC/TC_	TCC
5	173	M	R	K	ATG	AGG	AAG
11	422	S	T	T	TCC	ACA	ACC
21	898	C	C	C	TGC	TGT	TGC
21	905	F	F	L	TTT	TTC	TTA
24	1041	S	S	S	TCA	TCA	TCG
24	1042	S	S	S	TCC	TCC	TCA
28	1333	D	D	E	GAC	GAC	GAG
28	1349	Y	Y	Y	TAT	TAT	TAC*
42	2381	P	L	P	CCC	CTG	CCG
43	2479	S	S	S	TCG	TCG	TCA
45	2555	P	P	P	CCC	CCC	CCG
47	2591	P	P	P	CCC	CCT	CCC
49	2672	D	D	D	GAT	GAT	GAC
51	2744	E	E	E	GAG	GAG	GAA

[1]Amino acid residue position
[2]Untranslated region
[3]Nucleotide position
[4]Not Applicable
[5]Frameshift mutation
Boxed residues show amino acid differences between breeds
*This site has been shown to be polymorphic in some breeds
The mature VWF protein begins in exon 18

The alleles, as typed by both the *Bsi*E I and *Sau*96 I tests, showed no inconsistencies with Mendelian inheritance. One of these pedigrees included two affected animals, two phenotypically normal siblings, and the obligate carrier parents. The two parents were found to be heterozygous by the test, the two affected animals were found to be homozygous for the mutant allele, and the normal siblings were found to be heterozygotes.

Population survey for the mutation. Cheek swabs or blood samples were collected from 87 animals in order to determine the incidence of carriers in the U.S. Scottish terrier population. Although we attempted to make the sample as random as possible, these dogs were found to come from 16 pedigrees, several of which are more distantly interconnected. This is due to some ascertainment bias, based on ownership (as opposed to phenotypic ascertainment bias). In these 87 animals four affected and 15 carrier animals were found.

Discussion

These results establish that the single base deletion found in exon four of the vWF gene causes vWD in the Scottish terrier breed. The protein produced from the mutant allele is extremely short and does not include any of the mature vWF protein. Four Scottish terriers known to be affected with the disease are homozygous for the mutation. Five other mixed-breed dogs descended from Scottish terriers, and affected with vWD, are also homozygous for the mutation. No normal animals are homozygous for the mutation. Unaffected obligate carriers are always heterozygous for the mutation.

The gene frequency, as determined from the population survey, appears to be around 0.13 resulting in a heterozygote frequency of about 23% and expected frequency of affected animals of about 2%. Although the sample size is relatively small and somewhat biased, these data are in general agreement with the protein-based surveys (Stokol, T. et al., *Res Vet Sci* 59:152-155 (1995); Brooks, M., *Probl In Vet Med* 4:636-646 (1992)), in that the allele frequency is substantial.

All data collected thus far indicate that this mutation accounts for essentially all of the von Willebrand's disease found in Scottish terriers. This result is consistent with the results found for other genetic diseases, defined at the molecular level, in various domestic animals (Shuster, D.E. et al., *PNAS (USA)* 89:9225-9229 (1992); Rudolph, J.A. et al., *Nat Genet* 2:144-147 (1992); O'Brien, P.J. et al., *JAVMA* 203:842-851 (1993)). A likely explanation may be found in the pronounced founder effect that occurs in domestic animals, compared to most human and wild animal populations.

Published data using the protein-based factor assays have shown that, at least in several instances, obligate carriers have had factor levels that would lead to a diagnosis of "clear" of the disease allele. For example, in one study an obligate carrier had a factor level of 78% (Johnson, G.S. et al., *JAVMA* 176:1261-1263 (1980)). In another study, at least some of the obligate carriers had factor levels of

65% or greater (Brinkhous, K.M. et al., *Ann. New York Acad. Sci.* 370:191-203 (1981)). In addition, the number of animals that fall into an equivocal range can be substantial. In one study, 19% of Scottish terriers fell in this range (50-65% of the normal vWF antigen level) (Stokol, T. et al., *Res Vet Sci* 59:152-155 (1995)). Thus, although the protein-based tests have been useful, the certainty of the DNA-based test described herein should relieve the necessity of repeated testing and the variability associated with the protein-based assays.

The mutation is present in the pre-vWF part of the molecule. This part of the molecule is processed off prior to delivery of the mature protein into the plasma. This pre-portion of the molecule is important for the assembly of the mature vWF protein (Verwiej, L. et al., *EBMO J* 6:2885-2890 (1987); Wise, R.J. et al., *Cell* 52:229-236 (1988)). With the Scottish terrier frameshift vWD mutation, neither this pre-portion nor any of the mature factor is ever produced, in keeping with the fact that no factor has ever been detected in the blood of affected dogs.

The determination of the complete canine vWF cDNA sequence will have an impact upon the development of carrier tests for other breeds and other species as well. Currently, Shetland sheepdogs and Dutch Kooikers are known to have a significant amount of Type 3 vWD (Brooks, M. et al., *JAVMA* 200:1123-1127 (1992); Slappendel, R.J., *Vet-Q* 17:S21-S22 (1995)). Type 3 vWD has occasionally be seen in other breeds as well (*e.g.*, Johnson, G.S. et al., *JAVMA* 176:1261-1263 (1980)). All Type 3 vWD mutations described in humans to date have been found within the vWF gene itself. The availability of the canine sequence will make it easier to find the mutations in these breeds. In addition, at least some Type 1 mutations have been found within the human vWF gene, and thus Type 1 mutations may also be found within the vWF gene for breeds affected with that form of the disease. The availability of two divergent mammalian vWF cDNA sequences will also make it much easier to sequence the gene from other mammalian species using cross-species PCR methods (*e.g.*, Venta et al., *Biochem. Genet.* (1996) in press).

The test described herein for the detection of the mutation in Scottish terriers may be performed on small amounts of DNA from any tissue. The tissues that are the least invasive to obtain are blood and buccal cells. For maximum convenience, a cheek swab as a source of DNA is preferred.

The foregoing discussion discloses and describes merely exemplary embodiments of the present invention. One skilled in the art will readily recognize from such discussion, and from the accompanying drawings, that various changes,

modifications and variations can be made therein without departing from the spirit and scope of the invention.

All patents and other publications cited herein are expressly incorporated by reference.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Venta, Patrick J
Yuzbasiyan-Gurkan, Vilma
Schall, William D
Brewer, George J

(ii) TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Troy
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
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(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
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(C) TELEX: 287637

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8802 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 203..8641
(D) OTHER INFORMATION: /function= "Blood Clotting Protein"
/product= "Canine von Willebrand Factor"
/standard_name= "vWF"

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Venta, Patrick J.
Li, Jianping
Yuzbasiyan-Gurkan, Vilma
Schall, William D.
Brewer, George J.
(B) TITLE: Von Willebrand's Disease in the Scottish Terrier is Caused by a Single Base Deletion in Exon Four of the von Willebrand Factor Gene
(C) JOURNAL: Journal of the American Veterinary Medicine Association
(G) DATE: 1996
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 8802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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30 35 40

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45 50 55

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60 65 70

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95 100 105

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Gln Ser Ile Ser Met Pro Tyr Ala Ser Asn Gly Leu Tyr Leu Glu Ala
110 115 120

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125 130 135

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140 145 150

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Phe Ala Asn Ser Trp Ala Leu Ser Ser Gly Glu Gln Arg Cys Lys Arg
            190                 195                 200

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Val Ser Pro Pro Ser Ser Pro Cys Asn Val Ser Ser Asp Glu Val Gln
        205                 210                 215

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Gln Val Leu Trp Glu Gln Cys Gln Leu Leu Lys Ser Ala Ser Val Phe
    220                 225                 230

GCC CGC TGC CAC CCG CTG GTG GAC CCT GAG CCT TTT GTC GCC CTG TGT      952
Ala Arg Cys His Pro Leu Val Asp Pro Glu Pro Phe Val Ala Leu Cys
235                 240                 245                 250

GAA AGG ACT CTG TGC ACC TGT GTC CAG GGG ATG GAG TGC CCT TGT GCG     1000
Glu Arg Thr Leu Cys Thr Cys Val Gln Gly Met Glu Cys Pro Cys Ala
                255                 260                 265

GTC CTC CTG GAG TAC GCC CGG GCC TGT GCC CAG CAG GGG ATT GTC TTG     1048
Val Leu Leu Glu Tyr Ala Arg Ala Cys Ala Gln Gln Gly Ile Val Leu
            270                 275                 280

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Tyr Gly Trp Thr Asp His Ser Val Cys Arg Pro Ala Cys Pro Ala Gly
        285                 290                 295

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Met Glu Tyr Lys Glu Cys Val Ser Pro Cys Thr Arg Thr Cys Gln Ser
    300                 305                 310

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Leu His Val Lys Glu Val Cys Gln Glu Gln Cys Val Asp Gly Cys Ser
315                 320                 325                 330

TGC CCC GAG GGC CAG CTC CTG GAT GAA GGC CAC TGC GTG GGA AGT GCT     1240
Cys Pro Glu Gly Gln Leu Leu Asp Glu Gly His Cys Val Gly Ser Ala
                335                 340                 345

GAG TGT TCC TGT GTG CAT GCT GGG CAA CGG TAC CCT CCG GGC GCC TCC     1288
Glu Cys Ser Cys Val His Ala Gly Gln Arg Tyr Pro Pro Gly Ala Ser
            350                 355                 360

CTC TTA CAG GAC TGC CAC ACC TGC ATT TGC CGA AAT AGC CTG TGG ATC     1336
Leu Leu Gln Asp Cys His Thr Cys Ile Cys Arg Asn Ser Leu Trp Ile
        365                 370                 375

TGC AGC AAT GAA GAA TGC CCA GGC GAG TGT CTG GTC ACA GGA CAG TCC     1384
Cys Ser Asn Glu Glu Cys Pro Gly Glu Cys Leu Val Thr Gly Gln Ser
    380                 385                 390

CAC TTC AAG AGC TTC GAC AAC AGG TAC TTC ACC TTC AGT GGG GTC TGC     1432
His Phe Lys Ser Phe Asp Asn Arg Tyr Phe Thr Phe Ser Gly Val Cys
395                 400                 405                 410

CAC TAC CTG CTG GCC CAG GAC TGC CAG GAC CAC ACA TTC TCT GTT GTC     1480
His Tyr Leu Leu Ala Gln Asp Cys Gln Asp His Thr Phe Ser Val Val
                415                 420                 425

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Ile Glu Thr Val Gln Cys Ala Asp Asp Leu Asp Ala Val Cys Thr Arg
            430                 435                 440
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        445                 450                 455

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Lys Asn Gly Gly Gly Val Ser Met Asp Gly Gln Asp Ile Gln Ile Pro
    460                 465                 470

CTC CTG CAA GGT GAC CTC CGC ATC CAG CAC ACC GTG ATG GCC TCC GTG     1672
Leu Leu Gln Gly Asp Leu Arg Ile Gln His Thr Val Met Ala Ser Val
475                 480                 485                 490

CGC CTC AGC TAC GGG GAG GAC CTG CAG ATG GAT TCG GAC GTC CGG GGC     1720
Arg Leu Ser Tyr Gly Glu Asp Leu Gln Met Asp Ser Asp Val Arg Gly
                495                 500                 505

AGG CTA CTG GTG ACG CTG TAC CCC GCC TAC GCG GGG AAG ACG TGC GGC     1768
Arg Leu Leu Val Thr Leu Tyr Pro Ala Tyr Ala Gly Lys Thr Cys Gly
            510                 515                 520

CGT GGC GGG AAC TAC AAC GGC AAC CGG GGG GAC GAC TTC GTG ACG CCC     1816
Arg Gly Gly Asn Tyr Asn Gly Asn Arg Gly Asp Asp Phe Val Thr Pro
        525                 530                 535

GCA GGC CTG GCG GAG CCC CTG GTG GAG GAC TTC GGG AAC GCC TGG AAG     1864
Ala Gly Leu Ala Glu Pro Leu Val Glu Asp Phe Gly Asn Ala Trp Lys
    540                 545                 550

CTG CTC GGG GCC TGC GAG AAC CTG CAG AAG CAG CAC CGC GAT CCC TGC     1912
Leu Leu Gly Ala Cys Glu Asn Leu Gln Lys Gln His Arg Asp Pro Cys
555                 560                 565                 570

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Ser Leu Asn Pro Arg Gln Ala Arg Phe Ala Glu Glu Ala Cys Ala Leu
                575                 580                 585

CTG ACG TCC TCG AAG TTC GAG CCC TGC CAC CGA GCG GTG GGT CCT CAG     2008
Leu Thr Ser Ser Lys Phe Glu Pro Cys His Arg Ala Val Gly Pro Gln
            590                 595                 600

CCC TAC GTG CAG AAC TGC CTC TAC GAC GTC TGC TCC TGC TCC GAC GGC     2056
Pro Tyr Val Gln Asn Cys Leu Tyr Asp Val Cys Ser Cys Ser Asp Gly
        605                 610                 615

AGA GAC TGT CTT TGC AGC GCC GTG GCC AAC TAC GCC GCA GCC GTG GCC     2104
Arg Asp Cys Leu Cys Ser Ala Val Ala Asn Tyr Ala Ala Ala Val Ala
    620                 625                 630

CGG AGG GGC GTG CAC ATC GCG TGG CGG GAG CCG GGC TTC TGT GCG CTG     2152
Arg Arg Gly Val His Ile Ala Trp Arg Glu Pro Gly Phe Cys Ala Leu
635                 640                 645                 650

AGC TGC CCC CAG GGC CAG GTG TAC CTG CAG TGT GGG ACC CCC TGC AAC     2200
Ser Cys Pro Gln Gly Gln Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn
                655                 660                 665

ATG ACC TGT CTC TCC CTC TCT TAC CCG GAG GAG GAC TGC AAT GAG GTC     2248
Met Thr Cys Leu Ser Leu Ser Tyr Pro Glu Glu Asp Cys Asn Glu Val
            670                 675                 680

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Cys Leu Glu Ser Cys Phe Ser Pro Pro Gly Leu Tyr Leu Asp Glu Arg
        685                 690                 695

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    700                 705                 710
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715                 720                 725                 730

TGT GAG GAT GGC TTC ATG CAC TGT ACC ACA AGT GGA GGC CTG GGA AGC     2440
Cys Glu Asp Gly Phe Met His Cys Thr Thr Ser Gly Gly Leu Gly Ser
                735                 740                 745

CTG CTG CCC AAC CCG GTG CTC AGC AGC CCC CGG TGT CAC CGC AGC AAA     2488
Leu Leu Pro Asn Pro Val Leu Ser Ser Pro Arg Cys His Arg Ser Lys
            750                 755                 760

AGG AGC CTG TCC TGT CGG CCC CCC ATG GTC AAG TTG GTG TGT CCC GCT     2536
Arg Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala
        765                 770                 775

GAT AAC CCG AGG GCT GAA GGA CTG GAG TGT GCC AAA ACC TGC CAG AAC     2584
Asp Asn Pro Arg Ala Glu Gly Leu Glu Cys Ala Lys Thr Cys Gln Asn
    780                 785                 790

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Tyr Asp Leu Gln Cys Met Ser Thr Gly Cys Val Ser Gly Cys Leu Cys
795                 800                 805                 810

CCG CAG GGC ATG GTC CGG CAT GAA AAC AGG TGT GTG GCG CTG GAA AGA     2680
Pro Gln Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg
                815                 820                 825

TGT CCC TGC TTC CAC CAA GGC CAA GAG TAC GCC CCA GGA GAA ACC GTG     2728
Cys Pro Cys Phe His Gln Gly Gln Glu Tyr Ala Pro Gly Glu Thr Val
            830                 835                 840

AAA ATT GAC TGC AAC ACT TGT GTC TGT CGG GAC CGG AAG TGG ACC TGC     2776
Lys Ile Asp Cys Asn Thr Cys Val Cys Arg Asp Arg Lys Trp Thr Cys
        845                 850                 855

ACA GAC CAT GTG TGT GAT GCC ACT TGC TCT GCC ATC GGC ATG GCG CAC     2824
Thr Asp His Val Cys Asp Ala Thr Cys Ser Ala Ile Gly Met Ala His
    860                 865                 870

TAC CTC ACC TTC GAC GGA CTC AAG TAC CTG TTC CCT GGG GAG TGC CAG     2872
Tyr Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln
875                 880                 885                 890

TAT GTT CTG GTG CAG GAT TAC TGC GGC AGT AAC CCT GGG ACC TTA CGG     2920
Tyr Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Leu Arg
                895                 900                 905

ATC CTG GTG GGG AAC GAG GGG TGC AGC TAC CCC TCA GTG AAA TGC AAG     2968
Ile Leu Val Gly Asn Glu Gly Cys Ser Tyr Pro Ser Val Lys Cys Lys
            910                 915                 920

AAG CGG GTC ACC ATC CTG GTG GAA GGA GGA GAG ATT GAA CTG TTT GAT     3016
Lys Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp
        925                 930                 935

GGG GAG GTG AAT GTG AAG AAA CCC ATG AAG GAT GAG ACT CAC TTT GAG     3064
Gly Glu Val Asn Val Lys Lys Pro Met Lys Asp Glu Thr His Phe Glu
    940                 945                 950

GTG GTA GAG TCT GGT CAG TAC GTC ATT CTG CTG CTG GGC AAG GCA CTC     3112
Val Val Glu Ser Gly Gln Tyr Val Ile Leu Leu Leu Gly Lys Ala Leu
955                 960                 965                 970

TCT GTG GTC TGG GAC CAC CGC CTG AGC ATC TCT GTG ACC CTG AAG CGG     3160
Ser Val Val Trp Asp His Arg Leu Ser Ile Ser Val Thr Leu Lys Arg
                975                 980                 985
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Gln Asn Asn Asp Phe Thr Ser Ser Ser Leu Gln Ile Glu Glu Asp Pro
1005 1010 1015

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Val Asp Phe Gly Asn Ser Trp Lys Val Asn Pro Gln Cys Ala Asp Thr
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1135 1140 1145

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Leu Ala Cys Pro Val Gln Cys Val Glu Gly Cys His Ala His Cys Pro
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TGT GAT GGT GTC AAC TTC ACC TGT AAG GCC TGC AGA GAA CCC GGA AGT 3928
Cys Asp Gly Val Asn Phe Thr Cys Lys Ala Cys Arg Glu Pro Gly Ser
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GCC TCC ACC AGT GAG GTC TTA AAG TAC ACG CTG TTC CAG ATC TTT GGC 4312
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1375 1380 1385

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1390 1395 1400

GGC CTG AAG AAG AAG AAA GTC ATT GTC ATC CCT GTG GGC ATC GGG CCC 4456
Gly Leu Lys Lys Lys Lys Val Ile Val Ile Pro Val Gly Ile Gly Pro
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His Ala Ser Leu Lys Gln Ile His Leu Ile Glu Lys Gln Ala Pro Glu
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Asn Lys Ala Phe Val Phe Ser Gly Val Asp Glu Leu Glu Gln Arg Arg
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Val Val Phe Val Leu Glu Gly Ser Asp Lys Ile Gly Glu Ala Asn Phe
1500 1505 1510

AAC AAA AGC AGG GAG TTC ATG GAG GAG GTG ATT CAG CGG ATG GAC GTG 4792
Asn Lys Ser Arg Glu Phe Met Glu Glu Val Ile Gln Arg Met Asp Val
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GGC CAG GAC AGG ATC CAC GTC ACA GTG CTG CAG TAC TCG TAC ATG GTG 4840
Gly Gln Asp Arg Ile His Val Thr Val Leu Gln Tyr Ser Tyr Met Val
1535 1540 1545

ACC GTG GAG TAC ACC TTC AGC GAG GCG CAG TCC AAG GGC GAG GTC CTA 4888
Thr Val Glu Tyr Thr Phe Ser Glu Ala Gln Ser Lys Gly Glu Val Leu
1550 1555 1560

CAG CAG GTG CGG GAT ATC CGA TAC CGG GGT GGC AAC AGG ACC AAC ACT 4936
Gln Gln Val Arg Asp Ile Arg Tyr Arg Gly Gly Asn Arg Thr Asn Thr
1565 1570 1575

GGA CTG GCC CTG CAA TAC CTG TCC GAA CAC AGC TTC TCG GTC AGC CAG 4984
Gly Leu Ala Leu Gln Tyr Leu Ser Glu His Ser Phe Ser Val Ser Gln
1580 1585 1590

GGG GAC CGG GAG CAG GTA CCT AAC CTG GTC TAC ATG GTC ACA GGA AAC 5032
Gly Asp Arg Glu Gln Val Pro Asn Leu Val Tyr Met Val Thr Gly Asn
1595 1600 1605 1610

CCC GCT TCT GAT GAG ATC AAG CGG ATG CCT GGA GAC ATC CAG GTG GTG 5080
Pro Ala Ser Asp Glu Ile Lys Arg Met Pro Gly Asp Ile Gln Val Val
1615 1620 1625

CCC ATC GGG GTG GGT CCA CAT GCC AAT GTG CAG GAG CTG GAG AAG ATT 5128
Pro Ile Gly Val Gly Pro His Ala Asn Val Gln Glu Leu Glu Lys Ile
1630 1635 1640

GGC TGG CCC AAT GCC CCC ATC CTC ATC CAT GAC TTT GAG ATG CTC CCT 5176
Gly Trp Pro Asn Ala Pro Ile Leu Ile His Asp Phe Glu Met Leu Pro
1645 1650 1655

CGA GAG GCT CCT GAT CTG GTG CTA CAG AGG TGC TGC TCT GGA GAG GGG 5224
Arg Glu Ala Pro Asp Leu Val Leu Gln Arg Cys Cys Ser Gly Glu Gly
1660 1665 1670

CTG CAG ATC CCC ACC CTC TCC CCC ACC CCA GAT TGC AGC CAG CCC CTG 5272
Leu Gln Ile Pro Thr Leu Ser Pro Thr Pro Asp Cys Ser Gln Pro Leu
1675 1680 1685 1690

GAT GTG GTC CTC CTC CTG GAT GGC TCT TCC AGC ATT CCA GCT TCT TAC 5320
Asp Val Val Leu Leu Leu Asp Gly Ser Ser Ser Ile Pro Ala Ser Tyr
1695 1700 1705

TTT GAT GAA ATG AAG AGC TTC ACC AAG GCT TTT ATT TCA AGA GCT AAT 5368
Phe Asp Glu Met Lys Ser Phe Thr Lys Ala Phe Ile Ser Arg Ala Asn
1710 1715 1720

ATA GGG CCC CGG CTC ACT CAA GTG TCG GTG CTG CAA TAT GGA AGC ATC 5416
Ile Gly Pro Arg Leu Thr Gln Val Ser Val Leu Gln Tyr Gly Ser Ile
1725 1730 1735

ACC ACT ATC GAT GTG CCT TGG AAT GTA GCC TAT GAG AAA GTC CAT TTA 5464
Thr Thr Ile Asp Val Pro Trp Asn Val Ala Tyr Glu Lys Val His Leu
1740 1745 1750

CTG AGC CTT GTG GAC CTC ATG CAG CAG GAG GGA GGC CCC AGC GAA ATT 5512
Leu Ser Leu Val Asp Leu Met Gln Gln Glu Gly Gly Pro Ser Glu Ile
1755 1760 1765 1770

GGG GAT GCT TTG AGC TTT GCC GTG CGA TAT GTC ACC TCA GAA GTC CAT 5560
Gly Asp Ala Leu Ser Phe Ala Val Arg Tyr Val Thr Ser Glu Val His
1775 1780 1785

GGT GCC AGG CCC GGA GCC TCG AAA GCG GTG GTT ATC CTA GTC ACA GAT 5608
Gly Ala Arg Pro Gly Ala Ser Lys Ala Val Val Ile Leu Val Thr Asp
1790 1795 1800

GTC TCC GTG GAT TCA GTG GAT GCT GCA GCC GAG GCC GCC AGA TCC AAC 5656
Val Ser Val Asp Ser Val Asp Ala Ala Ala Glu Ala Ala Arg Ser Asn
1805 1810 1815

CGA GTG ACA GTG TTC CCC ATT GGA ATC GGG GAT CGG TAC AGT GAG GCC 5704
Arg Val Thr Val Phe Pro Ile Gly Ile Gly Asp Arg Tyr Ser Glu Ala
1820 1825 1830

CAG CTG AGC AGC TTG GCA GGC CCA AAG GCT GGC TCC AAT ATG GTA AGG 5752
Gln Leu Ser Ser Leu Ala Gly Pro Lys Ala Gly Ser Asn Met Val Arg
1835 1840 1845 1850

CTC CAG CGA ATT GAA GAC CTC CCC ACC GTG GCC ACC CTG GGA AAT TCC 5800
Leu Gln Arg Ile Glu Asp Leu Pro Thr Val Ala Thr Leu Gly Asn Ser
1855 1860 1865

TTC TTC CAC AAG CTG TGC TCT GGG TTT GAT AGA GTT TGC GTG GAT GAG 5848
Phe Phe His Lys Leu Cys Ser Gly Phe Asp Arg Val Cys Val Asp Glu
1870 1875 1880

GAT GGG AAT GAG AAG AGG CCC GGG GAT GTC TGG ACC TTG CCA GAC CAG 5896
Asp Gly Asn Glu Lys Arg Pro Gly Asp Val Trp Thr Leu Pro Asp Gln
1885 1890 1895

TGC CAC ACA GTG ACT TGC CTG CCA GAT GGC CAG ACC TTG CTG AAG AGT 5944
Cys His Thr Val Thr Cys Leu Pro Asp Gly Gln Thr Leu Leu Lys Ser
1900 1905 1910

CAT CGG GTC AAC TGT GAC CGG GGG CCA AGG CCT TCG TGC CCC AAT GGC 5992
His Arg Val Asn Cys Asp Arg Gly Pro Arg Pro Ser Cys Pro Asn Gly
1915 1920 1925 1930

CAG CCC CCT CTC AGG GTA GAG GAG ACC TGT GGC TGC CGC TGG ACC TGT 6040
Gln Pro Pro Leu Arg Val Glu Glu Thr Cys Gly Cys Arg Trp Thr Cys
1935 1940 1945

CCC TGT GTG TGC ATG GGC AGC TCT ACC CGG CAC ATC GTG ACC TTT GAT 6088
Pro Cys Val Cys Met Gly Ser Ser Thr Arg His Ile Val Thr Phe Asp
1950 1955 1960

GGG CAG AAT TTC AAG CTG ACT GGC AGC TGT TCG TAT GTC CTA TTT CAA 6136
Gly Gln Asn Phe Lys Leu Thr Gly Ser Cys Ser Tyr Val Leu Phe Gln
1965 1970 1975

AAC AAG GAG CAG GAC CTG GAG GTG ATT CTC CAG AAT GGT GCC TGC AGC 6184
Asn Lys Glu Gln Asp Leu Glu Val Ile Leu Gln Asn Gly Ala Cys Ser
1980 1985 1990

CCT GGG GCG AAG GAG ACC TGC ATG AAA TCC ATT GAG GTG AAG CAT GAC 6232
Pro Gly Ala Lys Glu Thr Cys Met Lys Ser Ile Glu Val Lys His Asp
1995 2000 2005 2010

GGC CTC TCA GTT GAG CTC CAC AGT GAC ATG CAG ATG ACA GTG AAT GGG 6280
Gly Leu Ser Val Glu Leu His Ser Asp Met Gln Met Thr Val Asn Gly
2015 2020 2025

AGA CTA GTC TCC ATC CCA TAT GTG GGT GGA GAC ATG GAA GTC AAT GTT 6328
Arg Leu Val Ser Ile Pro Tyr Val Gly Gly Asp Met Glu Val Asn Val
2030 2035 2040

TAT GGG ACC ATC ATG TAT GAG GTC AGA TTC AAC CAT CTT GGC CAC ATC 6376
Tyr Gly Thr Ile Met Tyr Glu Val Arg Phe Asn His Leu Gly His Ile
2045 2050 2055

TTC ACA TTC ACC CCC CAA AAC AAT GAG TTC CAG CTG CAG CTC AGC CCC 6424
Phe Thr Phe Thr Pro Gln Asn Asn Glu Phe Gln Leu Gln Leu Ser Pro
2060 2065 2070

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AGG ACC TTT GCT TCG AAG ACA TAT GGT CTC TGT GGG ATC TGT GAT GAG      6472
Arg Thr Phe Ala Ser Lys Thr Tyr Gly Leu Cys Gly Ile Cys Asp Glu
2075                2080                2085                2090

AAC GGA GCC AAT GAC TTC ATT CTG AGG GAT GGG ACA GTC ACC ACA GAC      6520
Asn Gly Ala Asn Asp Phe Ile Leu Arg Asp Gly Thr Val Thr Thr Asp
                2095                2100                2105

TGG AAG GCA CTC ATC CAG GAA TGG ACC GTA CAG CAG CTT GGG AAG ACA      6568
Trp Lys Ala Leu Ile Gln Glu Trp Thr Val Gln Gln Leu Gly Lys Thr
            2110                2115                2120

TCC CAG CCT GTC CAT GAG GAG CAG TGT CCT GTC TCC GAA TTC TTC CAC      6616
Ser Gln Pro Val His Glu Glu Gln Cys Pro Val Ser Glu Phe Phe His
        2125                2130                2135

TGC CAG GTC CTC CTC TCA GAA TTG TTT GCC GAG TGC CAC AAG GTC CTC      6664
Cys Gln Val Leu Leu Ser Glu Leu Phe Ala Glu Cys His Lys Val Leu
    2140                2145                2150

GCT CCA GCC ACC TTT TAT GCC ATG TGC CAG CCC GAC AGT TGC CAC CCG      6712
Ala Pro Ala Thr Phe Tyr Ala Met Cys Gln Pro Asp Ser Cys His Pro
2155                2160                2165                2170

AAG AAA GTG TGT GAG GCG ATT GCC TTG TAT GCC CAC CTC TGT CGG ACC      6760
Lys Lys Val Cys Glu Ala Ile Ala Leu Tyr Ala His Leu Cys Arg Thr
                2175                2180                2185

AAA GGG GTC TGT GTG GAC TGG AGG AGG GCC AAT TTC TGT GCT ATG TCA      6808
Lys Gly Val Cys Val Asp Trp Arg Arg Ala Asn Phe Cys Ala Met Ser
            2190                2195                2200

TGT CCA CCA TCC CTG GTG TAC AAC CAC TGT GAG CAT GGC TGC CCT CGG      6856
Cys Pro Pro Ser Leu Val Tyr Asn His Cys Glu His Gly Cys Pro Arg
        2205                2210                2215

CTC TGT GAA GGC AAT ACA AGC TCC TGT GGG GAC CAA CCC TCG GAA GGC      6904
Leu Cys Glu Gly Asn Thr Ser Ser Cys Gly Asp Gln Pro Ser Glu Gly
    2220                2225                2230

TGC TTC TGC CCC CCA AAC CAA GTC ATG CTG GAA GGT AGC TGT GTC CCC      6952
Cys Phe Cys Pro Pro Asn Gln Val Met Leu Glu Gly Ser Cys Val Pro
2235                2240                2245                2250

GAG GAG GCC TGT ACC CAG TGC ATC AGC GAG GAT GGA GTC CGG CAC CAG      7000
Glu Glu Ala Cys Thr Gln Cys Ile Ser Glu Asp Gly Val Arg His Gln
                2255                2260                2265

TTC CTG GAA ACC TGG GTC CCA GCC CAC CAG CCT TGC CAG ATC TGC ACG      7048
Phe Leu Glu Thr Trp Val Pro Ala His Gln Pro Cys Gln Ile Cys Thr
            2270                2275                2280

TGC CTC AGT GGG CGG AAG GTC AAC TGT ACG TTG CAG CCC TGC CCC ACA      7096
Cys Leu Ser Gly Arg Lys Val Asn Cys Thr Leu Gln Pro Cys Pro Thr
        2285                2290                2295

GCC AAA GCT CCC ACC TGT GGC CCG TGT GAA GTG GCC CGC CTC CGC CAG      7144
Ala Lys Ala Pro Thr Cys Gly Pro Cys Glu Val Ala Arg Leu Arg Gln
    2300                2305                2310

AAC GCA GTG CAG TGC TGC CCG GAG TAC GAG TGT GTG TGT GAC CTG GTG      7192
Asn Ala Val Gln Cys Cys Pro Glu Tyr Glu Cys Val Cys Asp Leu Val
2315                2320                2325                2330

AGC TGT GAC CTG CCC CCG GTG CCT CCC TGC GAA GAT GGC CTC CAG ATG      7240
Ser Cys Asp Leu Pro Pro Val Pro Pro Cys Glu Asp Gly Leu Gln Met
                2335                2340                2345
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ACC CTG ACC AAT CCT GGC GAG TGC AGA CCC AAC TTC ACC TGT GCC TGC 7288
Thr Leu Thr Asn Pro Gly Glu Cys Arg Pro Asn Phe Thr Cys Ala Cys
2350 2355 2360

AGG AAG GAT GAA TGC AGA CGG GAG TCC CCG CCC TCT TGT CCC CCG CAC 7336
Arg Lys Asp Glu Cys Arg Arg Glu Ser Pro Pro Ser Cys Pro Pro His
2365 2370 2375

CGG ACG CCG GCC CTT CGG AAG ACT CAG TGC TGT GAT GAG TAT GAG TGT 7384
Arg Thr Pro Ala Leu Arg Lys Thr Gln Cys Cys Asp Glu Tyr Glu Cys
2380 2385 2390

GCA TGC AAC TGT GTC AAC TCC ACG GTG AGC TGC CCG CTT GGG TAC CTG 7432
Ala Cys Asn Cys Val Asn Ser Thr Val Ser Cys Pro Leu Gly Tyr Leu
2395 2400 2405 2410

GCC TCG GCT GTC ACC AAC GAC TGT GGC TGC ACC ACA ACA ACC TGC TTC 7480
Ala Ser Ala Val Thr Asn Asp Cys Gly Cys Thr Thr Thr Thr Cys Phe
2415 2420 2425

CCT GAC AAG GTG TGT GTC CAC CGA GGC ACC ATC TAC CCT GTG GGC CAG 7528
Pro Asp Lys Val Cys Val His Arg Gly Thr Ile Tyr Pro Val Gly Gln
2430 2435 2440

TTC TGG GAG GAG GCC TGT GAC GTG TGC ACC TGC ACG GAC TTG GAG GAC 7576
Phe Trp Glu Glu Ala Cys Asp Val Cys Thr Cys Thr Asp Leu Glu Asp
2445 2450 2455

TCT GTG ATG GGC CTG CGT GTG GCC CAG TGC TCC CAG AAG CCC TGT GAG 7624
Ser Val Met Gly Leu Arg Val Ala Gln Cys Ser Gln Lys Pro Cys Glu
2460 2465 2470

GAC AAC TGC CTG TCA GGC TTC ACT TAT GTC CTT CAT GAA GGC GAG TGC 7672
Asp Asn Cys Leu Ser Gly Phe Thr Tyr Val Leu His Glu Gly Glu Cys
2475 2480 2485 2490

TGT GGA AGG TGT CTG CCA TCT GCC TGT GAG GTG GTC ACT GGT TCA CCA 7720
Cys Gly Arg Cys Leu Pro Ser Ala Cys Glu Val Val Thr Gly Ser Pro
2495 2500 2505

CGG GGC GAC GCC CAG TCT CAC TGG AAG AAT GTT GGC TCT CAC TGG GCC 7768
Arg Gly Asp Ala Gln Ser His Trp Lys Asn Val Gly Ser His Trp Ala
2510 2515 2520

TCC CCT GAC AAC CCC TGC CTC ATC AAT GAG TGT GTC CGA GTG AAG GAA 7816
Ser Pro Asp Asn Pro Cys Leu Ile Asn Glu Cys Val Arg Val Lys Glu
2525 2530 2535

GAG GTC TTT GTG CAA CAG AGG AAT GTC TCC TGC CCC CAG CTG AAT GTC 7864
Glu Val Phe Val Gln Gln Arg Asn Val Ser Cys Pro Gln Leu Asn Val
2540 2545 2550

CCC ACC TGC CCC ACG GGC TTC CAG CTG AGC TGT AAG ACC TCA GAG TGT 7912
Pro Thr Cys Pro Thr Gly Phe Gln Leu Ser Cys Lys Thr Ser Glu Cys
2555 2560 2565 2570

TGT CCC ACC TGT CAC TGC GAG CCC CTG GAG GCC TGC TTG CTC AAT GGT 7960
Cys Pro Thr Cys His Cys Glu Pro Leu Glu Ala Cys Leu Leu Asn Gly
2575 2580 2585

ACC ATC ATT GGG CCG GGG AAA AGT CTG ATG ATT GAT GTG TGT ACA ACC 8008
Thr Ile Ile Gly Pro Gly Lys Ser Leu Met Ile Asp Val Cys Thr Thr
2590 2595 2600

TGC CGC TGC ACC GTG CCG GTG GGA GTC ATC TCT GGA TTC AAG CTG GAG 8056
Cys Arg Cys Thr Val Pro Val Gly Val Ile Ser Gly Phe Lys Leu Glu
2605 2610 2615

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GGC AGG AAG ACC ACC TGT GAG GCA TGC CCC CTG GGT TAT AAG GAA GAG      8104
Gly Arg Lys Thr Thr Cys Glu Ala Cys Pro Leu Gly Tyr Lys Glu Glu
    2620                2625                2630

AAG AAC CAA GGT GAA TGC TGT GGG AGA TGT CTG CCT ATA GCT TGC ACC      8152
Lys Asn Gln Gly Glu Cys Cys Gly Arg Cys Leu Pro Ile Ala Cys Thr
2635                2640                2645                2650

ATT CAG CTA AGA GGA GGA CAG ATC ATG ACA CTG AAG CGT GAT GAG ACT      8200
Ile Gln Leu Arg Gly Gly Gln Ile Met Thr Leu Lys Arg Asp Glu Thr
                2655                2660                2665

ATC CAG GAT GGC TGT GAC AGT CAC TTC TGC AAG GTC AAT GAA AGA GGA      8248
Ile Gln Asp Gly Cys Asp Ser His Phe Cys Lys Val Asn Glu Arg Gly
            2670                2675                2680

GAG TAC ATC TGG GAG AAG AGA GTC ACG GGT TGC CCA CCT TTC GAT GAA      8296
Glu Tyr Ile Trp Glu Lys Arg Val Thr Gly Cys Pro Pro Phe Asp Glu
        2685                2690                2695

CAC AAG TGT CTG GCT GAG GGA GGA AAA ATC ATG AAA ATT CCA GGC ACC      8344
His Lys Cys Leu Ala Glu Gly Gly Lys Ile Met Lys Ile Pro Gly Thr
    2700                2705                2710

TGC TGT GAC ACA TGT GAG GAG CCA GAA TGC AAG GAT ATC ATT GCC AAG      8392
Cys Cys Asp Thr Cys Glu Glu Pro Glu Cys Lys Asp Ile Ile Ala Lys
2715                2720                2725                2730

CTG CAG CGT GTC AAA GTG GGA GAC TGT AAG TCT GAA GAG GAA GTG GAC      8440
Leu Gln Arg Val Lys Val Gly Asp Cys Lys Ser Glu Glu Glu Val Asp
                2735                2740                2745

ATT CAT TAC TGT GAG GGT AAA TGT GCC AGC AAA GCC GTG TAC TCC ATC      8488
Ile His Tyr Cys Glu Gly Lys Cys Ala Ser Lys Ala Val Tyr Ser Ile
            2750                2755                2760

CAC ATG GAG GAT GTG CAG GAC CAG TGC TCC TGC TGC TCG CCC ACC CAG      8536
His Met Glu Asp Val Gln Asp Gln Cys Ser Cys Cys Ser Pro Thr Gln
        2765                2770                2775

ACG GAG CCC ATG CAG GTG GCC CTG CGC TGC ACC AAT GGC TCC CTC ATC      8584
Thr Glu Pro Met Gln Val Ala Leu Arg Cys Thr Asn Gly Ser Leu Ile
    2780                2785                2790

TAC CAT GAG ATC CTC AAT GCC ATC GAA TGC AGG TGT TCC CCC AGG AAG      8632
Tyr His Glu Ile Leu Asn Ala Ile Glu Cys Arg Cys Ser Pro Arg Lys
2795                2800                2805                2810

TGC AGC AAG TGAGGCCACT GCCTGGATGC TACTGTCGCC TGCCTTACCC              8681
Cys Ser Lys

GACCTCACTG GACTGGCCAG AGTGCTGCTC AGTCCTCCTC AGTCCTCCTC CTGCTCTGCT    8741

CTTGTGCTTC CTGATCCCAC AATAAAGGTC AATCTTTCAC CTTGAAAAAA AAAAAAAAAA    8801

A                                                                    8802
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2813 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ser Pro Thr Arg Leu Val Arg Val Leu Leu Ala Leu Ala Leu Ile
  1               5                  10                  15

Leu Pro Gly Lys Leu Cys Thr Lys Gly Thr Val Gly Arg Ser Ser Met
             20                  25                  30

Ala Arg Cys Ser Leu Leu Gly Gly Asp Phe Ile Asn Thr Phe Asp Glu
         35                  40                  45

Ser Met Tyr Ser Phe Ala Gly Asp Cys Ser Tyr Leu Leu Ala Gly Asp
     50                  55                  60

Cys Gln Glu His Ser Ile Ser Leu Ile Gly Gly Phe Gln Asn Asp Lys
 65                  70                  75                  80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
                 85                  90                  95

Phe Val Asn Gly Thr Met Leu Gln Gly Thr Gln Ser Ile Ser Met Pro
            100                 105                 110

Tyr Ala Ser Asn Gly Leu Tyr Leu Glu Ala Glu Ala Gly Tyr Tyr Lys
        115                 120                 125

Leu Ser Ser Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Asn Gly
    130                 135                 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145                 150                 155                 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Lys Thr Gln
                165                 170                 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
            180                 185                 190

Leu Ser Ser Gly Glu Gln Arg Cys Lys Arg Val Ser Pro Pro Ser Ser
        195                 200                 205

Pro Cys Asn Val Ser Ser Asp Glu Val Gln Gln Val Leu Trp Glu Gln
    210                 215                 220

Cys Gln Leu Leu Lys Ser Ala Ser Val Phe Ala Arg Cys His Pro Leu
225                 230                 235                 240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Arg Thr Leu Cys Thr
                245                 250                 255

Cys Val Gln Gly Met Glu Cys Pro Cys Ala Val Leu Leu Glu Tyr Ala
            260                 265                 270

Arg Ala Cys Ala Gln Gln Gly Ile Val Leu Tyr Gly Trp Thr Asp His
        275                 280                 285

Ser Val Cys Arg Pro Ala Cys Pro Ala Gly Met Glu Tyr Lys Glu Cys
    290                 295                 300

Val Ser Pro Cys Thr Arg Thr Cys Gln Ser Leu His Val Lys Glu Val
305                 310                 315                 320

Cys Gln Glu Gln Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
                325                 330                 335

Leu Asp Glu Gly His Cys Val Gly Ser Ala Glu Cys Ser Cys Val His
            340                 345                 350
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Ala Gly Gln Arg Tyr Pro Pro Gly Ala Ser Leu Leu Gln Asp Cys His
        355                 360                 365

Thr Cys Ile Cys Arg Asn Ser Leu Trp Ile Cys Ser Asn Glu Glu Cys
    370                 375                 380

Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
385                 390                 395                     400

Asn Arg Tyr Phe Thr Phe Ser Gly Val Cys His Tyr Leu Leu Ala Gln
                405                 410                     415

Asp Cys Gln Asp His Thr Phe Ser Val Val Ile Glu Thr Val Gln Cys
            420                 425                 430

Ala Asp Asp Leu Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
        435                 440                 445

Pro Gly His His Asn Ser Leu Val Lys Leu Lys Asn Gly Gly Gly Val
    450                 455                 460

Ser Met Asp Gly Gln Asp Ile Gln Ile Pro Leu Leu Gln Gly Asp Leu
465                 470                 475                     480

Arg Ile Gln His Thr Val Met Ala Ser Val Arg Leu Ser Tyr Gly Glu
                485                 490                     495

Asp Leu Gln Met Asp Ser Asp Val Arg Gly Arg Leu Leu Val Thr Leu
            500                 505                 510

Tyr Pro Ala Tyr Ala Gly Lys Thr Cys Gly Arg Gly Gly Asn Tyr Asn
        515                 520                 525

Gly Asn Arg Gly Asp Asp Phe Val Thr Pro Ala Gly Leu Ala Glu Pro
    530                 535                 540

Leu Val Glu Asp Phe Gly Asn Ala Trp Lys Leu Leu Gly Ala Cys Glu
545                 550                 555                     560

Asn Leu Gln Lys Gln His Arg Asp Pro Cys Ser Leu Asn Pro Arg Gln
                565                 570                     575

Ala Arg Phe Ala Glu Glu Ala Cys Ala Leu Leu Thr Ser Ser Lys Phe
            580                 585                 590

Glu Pro Cys His Arg Ala Val Gly Pro Gln Pro Tyr Val Gln Asn Cys
        595                 600                 605

Leu Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Asp Cys Leu Cys Ser
    610                 615                 620

Ala Val Ala Asn Tyr Ala Ala Ala Val Ala Arg Arg Gly Val His Ile
625                 630                 635                     640

Ala Trp Arg Glu Pro Gly Phe Cys Ala Leu Ser Cys Pro Gln Gly Gln
                645                 650                     655

Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Met Thr Cys Leu Ser Leu
            660                 665                 670

Ser Tyr Pro Glu Glu Asp Cys Asn Glu Val Cys Leu Glu Ser Cys Phe
        675                 680                 685

Ser Pro Pro Gly Leu Tyr Leu Asp Glu Arg Gly Asp Cys Val Pro Lys
    690                 695                 700
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Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705 710 715 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
725 730 735

His Cys Thr Thr Ser Gly Gly Leu Gly Ser Leu Leu Pro Asn Pro Val
740 745 750

Leu Ser Ser Pro Arg Cys His Arg Ser Lys Arg Ser Leu Ser Cys Arg
755 760 765

Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Pro Arg Ala Glu
770 775 780

Gly Leu Glu Cys Ala Lys Thr Cys Gln Asn Tyr Asp Leu Gln Cys Met
785 790 795 800

Ser Thr Gly Cys Val Ser Gly Cys Leu Cys Pro Gln Gly Met Val Arg
805 810 815

His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
820 825 830

Gly Gln Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Asp Cys Asn Thr
835 840 845

Cys Val Cys Arg Asp Arg Lys Trp Thr Cys Thr Asp His Val Cys Asp
850 855 860

Ala Thr Cys Ser Ala Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
865 870 875 880

Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
885 890 895

Tyr Cys Gly Ser Asn Pro Gly Thr Leu Arg Ile Leu Val Gly Asn Glu
900 905 910

Gly Cys Ser Tyr Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
915 920 925

Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
930 935 940

Lys Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Gln
945 950 955 960

Tyr Val Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp His
965 970 975

Arg Leu Ser Ile Ser Val Thr Leu Lys Arg Thr Tyr Gln Glu Gln Val
980 985 990

Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln Asn Asn Asp Phe Thr
995 1000 1005

Ser Ser Ser Leu Gln Ile Glu Glu Asp Pro Val Asp Phe Gly Asn Ser
1010 1015 1020

Trp Lys Val Asn Pro Gln Cys Ala Asp Thr Lys Lys Val Pro Leu Asp
1025 1030 1035 1040

Ser Ser Pro Ala Val Cys His Asn Asn Ile Met Lys Gln Thr Met Val
1045 1050 1055

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Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Ile Phe Gln Asp Cys Asn
            1060                1065                1070

Arg Leu Val Asp Pro Glu Pro Phe Leu Asp Ile Cys Ile Tyr Asp Thr
        1075                1080                1085

Cys Ser Cys Glu Ser Ile Gly Asp Cys Thr Cys Phe Cys Asp Thr Ile
    1090                1095                1100

Ala Ala Tyr Ala His Val Cys Ala Gln His Gly Lys Val Val Ala Trp
1105                1110                1115                1120

Arg Thr Ala Thr Phe Cys Pro Gln Asn Cys Glu Glu Arg Asn Leu His
                1125                1130                1135

Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn Ser Cys Ala Pro Ala
            1140                1145                1150

Cys Pro Ile Thr Cys Gln His Pro Glu Pro Leu Ala Cys Pro Val Gln
        1155                1160                1165

Cys Val Glu Gly Cys His Ala His Cys Pro Pro Gly Lys Ile Leu Asp
    1170                1175                1180

Glu Leu Leu Gln Thr Cys Ile Asp Pro Glu Asp Cys Pro Val Cys Glu
1185                1190                1195                1200

Val Ala Gly Arg Arg Leu Ala Pro Gly Lys Lys Ile Ile Leu Asn Pro
                1205                1210                1215

Ser Asp Pro Glu His Cys Gln Ile Cys Asn Cys Asp Gly Val Asn Phe
            1220                1225                1230

Thr Cys Lys Ala Cys Arg Glu Pro Gly Ser Val Val Val Pro Pro Thr
        1235                1240                1245

Asp Gly Pro Ile Gly Ser Thr Thr Ser Tyr Val Glu Asp Thr Ser Glu
    1250                1255                1260

Pro Pro Leu His Asp Phe His Cys Ser Arg Leu Leu Asp Leu Val Phe
1265                1270                1275                1280

Leu Leu Asp Gly Ser Ser Lys Leu Ser Glu Asp Glu Phe Glu Val Leu
                1285                1290                1295

Lys Val Phe Val Val Gly Met Met Glu His Leu His Ile Ser Gln Lys
            1300                1305                1310

Arg Ile Arg Val Ala Val Val Glu Tyr His Asp Gly Ser His Ala Tyr
        1315                1320                1325

Ile Glu Leu Lys Asp Arg Lys Arg Pro Ser Glu Leu Arg Arg Ile Thr
    1330                1335                1340

Ser Gln Val Lys Tyr Ala Gly Ser Glu Val Ala Ser Thr Ser Glu Val
1345                1350                1355                1360

Leu Lys Tyr Thr Leu Phe Gln Ile Phe Gly Lys Ile Asp Arg Pro Glu
                1365                1370                1375

Ala Ser Arg Ile Ala Leu Leu Leu Met Ala Ser Gln Glu Pro Ser Arg
            1380                1385                1390

Leu Ala Arg Asn Leu Val Arg Tyr Val Gln Gly Leu Lys Lys Lys Lys
        1395                1400                1405
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Val Ile Val Ile Pro Val Gly Ile Gly Pro His Ala Ser Leu Lys Gln
1410 1415 1420

Ile His Leu Ile Glu Lys Gln Ala Pro Glu Asn Lys Ala Phe Val Phe
1425 1430 1435 1440

Ser Gly Val Asp Glu Leu Glu Gln Arg Arg Asp Glu Ile Ile Asn Tyr
1445 1450 1455

Leu Cys Asp Leu Ala Pro Glu Ala Pro Ala Pro Thr Gln His Pro Pro
1460 1465 1470

Met Ala Gln Val Thr Val Gly Ser Glu Leu Leu Gly Val Ser Ser Pro
1475 1480 1485

Gly Pro Lys Arg Asn Ser Met Val Leu Asp Val Val Phe Val Leu Glu
1490 1495 1500

Gly Ser Asp Lys Ile Gly Glu Ala Asn Phe Asn Lys Ser Arg Glu Phe
1505 1510 1515 1520

Met Glu Glu Val Ile Gln Arg Met Asp Val Gly Gln Asp Arg Ile His
1525 1530 1535

Val Thr Val Leu Gln Tyr Ser Tyr Met Val Thr Val Glu Tyr Thr Phe
1540 1545 1550

Ser Glu Ala Gln Ser Lys Gly Glu Val Leu Gln Gln Val Arg Asp Ile
1555 1560 1565

Arg Tyr Arg Gly Gly Asn Arg Thr Asn Thr Gly Leu Ala Leu Gln Tyr
1570 1575 1580

Leu Ser Glu His Ser Phe Ser Val Ser Gln Gly Asp Arg Glu Gln Val
1585 1590 1595 1600

Pro Asn Leu Val Tyr Met Val Thr Gly Asn Pro Ala Ser Asp Glu Ile
1605 1610 1615

Lys Arg Met Pro Gly Asp Ile Gln Val Val Pro Ile Gly Val Gly Pro
1620 1625 1630

His Ala Asn Val Gln Glu Leu Glu Lys Ile Gly Trp Pro Asn Ala Pro
1635 1640 1645

Ile Leu Ile His Asp Phe Glu Met Leu Pro Arg Glu Ala Pro Asp Leu
1650 1655 1660

Val Leu Gln Arg Cys Cys Ser Gly Glu Gly Leu Gln Ile Pro Thr Leu
1665 1670 1675 1680

Ser Pro Thr Pro Asp Cys Ser Gln Pro Leu Asp Val Val Leu Leu Leu
1685 1690 1695

Asp Gly Ser Ser Ser Ile Pro Ala Ser Tyr Phe Asp Glu Met Lys Ser
1700 1705 1710

Phe Thr Lys Ala Phe Ile Ser Arg Ala Asn Ile Gly Pro Arg Leu Thr
1715 1720 1725

Gln Val Ser Val Leu Gln Tyr Gly Ser Ile Thr Thr Ile Asp Val Pro
1730 1735 1740

Trp Asn Val Ala Tyr Glu Lys Val His Leu Leu Ser Leu Val Asp Leu
1745 1750 1755 1760

Met Gln Gln Glu Gly Gly Pro Ser Glu Ile Gly Asp Ala Leu Ser Phe
1765 1770 1775

Ala Val Arg Tyr Val Thr Ser Glu Val His Gly Ala Arg Pro Gly Ala
1780 1785 1790

Ser Lys Ala Val Val Ile Leu Val Thr Asp Val Ser Val Asp Ser Val
1795 1800 1805

Asp Ala Ala Ala Glu Ala Ala Arg Ser Asn Arg Val Thr Val Phe Pro
1810 1815 1820

Ile Gly Ile Gly Asp Arg Tyr Ser Glu Ala Gln Leu Ser Ser Leu Ala
1825 1830 1835 1840

Gly Pro Lys Ala Gly Ser Asn Met Val Arg Leu Gln Arg Ile Glu Asp
1845 1850 1855

Leu Pro Thr Val Ala Thr Leu Gly Asn Ser Phe Phe His Lys Leu Cys
1860 1865 1870

Ser Gly Phe Asp Arg Val Cys Val Asp Glu Asp Gly Asn Glu Lys Arg
1875 1880 1885

Pro Gly Asp Val Trp Thr Leu Pro Asp Gln Cys His Thr Val Thr Cys
1890 1895 1900

Leu Pro Asp Gly Gln Thr Leu Leu Lys Ser His Arg Val Asn Cys Asp
1905 1910 1915 1920

Arg Gly Pro Arg Pro Ser Cys Pro Asn Gly Gln Pro Pro Leu Arg Val
1925 1930 1935

Glu Glu Thr Cys Gly Cys Arg Trp Thr Cys Pro Cys Val Cys Met Gly
1940 1945 1950

Ser Ser Thr Arg His Ile Val Thr Phe Asp Gly Gln Asn Phe Lys Leu
1955 1960 1965

Thr Gly Ser Cys Ser Tyr Val Leu Phe Gln Asn Lys Glu Gln Asp Leu
1970 1975 1980

Glu Val Ile Leu Gln Asn Gly Ala Cys Ser Pro Gly Ala Lys Glu Thr
1985 1990 1995 2000

Cys Met Lys Ser Ile Glu Val Lys His Asp Gly Leu Ser Val Glu Leu
2005 2010 2015

His Ser Asp Met Gln Met Thr Val Asn Gly Arg Leu Val Ser Ile Pro
2020 2025 2030

Tyr Val Gly Gly Asp Met Glu Val Asn Val Tyr Gly Thr Ile Met Tyr
2035 2040 2045

Glu Val Arg Phe Asn His Leu Gly His Ile Phe Thr Phe Thr Pro Gln
2050 2055 2060

Asn Asn Glu Phe Gln Leu Gln Leu Ser Pro Arg Thr Phe Ala Ser Lys
2065 2070 2075 2080

Thr Tyr Gly Leu Cys Gly Ile Cys Asp Glu Asn Gly Ala Asn Asp Phe
2085 2090 2095

Ile Leu Arg Asp Gly Thr Val Thr Thr Asp Trp Lys Ala Leu Ile Gln
2100 2105 2110

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Glu Trp Thr Val Gln Gln Leu Gly Lys Thr Ser Gln Pro Val His Glu
        2115                2120                2125

Glu Gln Cys Pro Val Ser Glu Phe Phe His Cys Gln Val Leu Leu Ser
    2130                2135                2140

Glu Leu Phe Ala Glu Cys His Lys Val Leu Ala Pro Ala Thr Phe Tyr
2145                2150                2155                2160

Ala Met Cys Gln Pro Asp Ser Cys His Pro Lys Lys Val Cys Glu Ala
                2165                2170                2175

Ile Ala Leu Tyr Ala His Leu Cys Arg Thr Lys Gly Val Cys Val Asp
            2180                2185                2190

Trp Arg Arg Ala Asn Phe Cys Ala Met Ser Cys Pro Pro Ser Leu Val
        2195                2200                2205

Tyr Asn His Cys Glu His Gly Cys Pro Arg Leu Cys Glu Gly Asn Thr
    2210                2215                2220

Ser Ser Cys Gly Asp Gln Pro Ser Glu Gly Cys Phe Cys Pro Pro Asn
2225                2230                2235                2240

Gln Val Met Leu Glu Gly Ser Cys Val Pro Glu Glu Ala Cys Thr Gln
                2245                2250                2255

Cys Ile Ser Glu Asp Gly Val Arg His Gln Phe Leu Glu Thr Trp Val
            2260                2265                2270

Pro Ala His Gln Pro Cys Gln Ile Cys Thr Cys Leu Ser Gly Arg Lys
        2275                2280                2285

Val Asn Cys Thr Leu Gln Pro Cys Pro Thr Ala Lys Ala Pro Thr Cys
    2290                2295                2300

Gly Pro Cys Glu Val Ala Arg Leu Arg Gln Asn Ala Val Gln Cys Cys
2305                2310                2315                2320

Pro Glu Tyr Glu Cys Val Cys Asp Leu Val Ser Cys Asp Leu Pro Pro
                2325                2330                2335

Val Pro Pro Cys Glu Asp Gly Leu Gln Met Thr Leu Thr Asn Pro Gly
            2340                2345                2350

Glu Cys Arg Pro Asn Phe Thr Cys Ala Cys Arg Lys Asp Glu Cys Arg
        2355                2360                2365

Arg Glu Ser Pro Pro Ser Cys Pro Pro His Arg Thr Pro Ala Leu Arg
    2370                2375                2380

Lys Thr Gln Cys Cys Asp Glu Tyr Glu Cys Ala Cys Asn Cys Val Asn
2385                2390                2395                2400

Ser Thr Val Ser Cys Pro Leu Gly Tyr Leu Ala Ser Ala Val Thr Asn
                2405                2410                2415

Asp Cys Gly Cys Thr Thr Thr Thr Cys Phe Pro Asp Lys Val Cys Val
            2420                2425                2430

His Arg Gly Thr Ile Tyr Pro Val Gly Gln Phe Trp Glu Glu Ala Cys
        2435                2440                2445

Asp Val Cys Thr Cys Thr Asp Leu Glu Asp Ser Val Met Gly Leu Arg
    2450                2455                2460
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Val Ala Gln Cys Ser Gln Lys Pro Cys Glu Asp Asn Cys Leu Ser Gly
2465 2470 2475 2480

Phe Thr Tyr Val Leu His Glu Gly Glu Cys Cys Gly Arg Cys Leu Pro
2485 2490 2495

Ser Ala Cys Glu Val Val Thr Gly Ser Pro Arg Gly Asp Ala Gln Ser
2500 2505 2510

His Trp Lys Asn Val Gly Ser His Trp Ala Ser Pro Asp Asn Pro Cys
2515 2520 2525

Leu Ile Asn Glu Cys Val Arg Val Lys Glu Glu Val Phe Val Gln Gln
2530 2535 2540

Arg Asn Val Ser Cys Pro Gln Leu Asn Val Pro Thr Cys Pro Thr Gly
2545 2550 2555 2560

Phe Gln Leu Ser Cys Lys Thr Ser Glu Cys Cys Pro Thr Cys His Cys
2565 2570 2575

Glu Pro Leu Glu Ala Cys Leu Leu Asn Gly Thr Ile Ile Gly Pro Gly
2580 2585 2590

Lys Ser Leu Met Ile Asp Val Cys Thr Thr Cys Arg Cys Thr Val Pro
2595 2600 2605

Val Gly Val Ile Ser Gly Phe Lys Leu Glu Gly Arg Lys Thr Thr Cys
2610 2615 2620

Glu Ala Cys Pro Leu Gly Tyr Lys Glu Glu Lys Asn Gln Gly Glu Cys
2625 2630 2635 2640

Cys Gly Arg Cys Leu Pro Ile Ala Cys Thr Ile Gln Leu Arg Gly Gly
2645 2650 2655

Gln Ile Met Thr Leu Lys Arg Asp Glu Thr Ile Gln Asp Gly Cys Asp
2660 2665 2670

Ser His Phe Cys Lys Val Asn Glu Arg Gly Glu Tyr Ile Trp Glu Lys
2675 2680 2685

Arg Val Thr Gly Cys Pro Pro Phe Asp Glu His Lys Cys Leu Ala Glu
2690 2695 2700

Gly Gly Lys Ile Met Lys Ile Pro Gly Thr Cys Cys Asp Thr Cys Glu
2705 2710 2715 2720

Glu Pro Glu Cys Lys Asp Ile Ile Ala Lys Leu Gln Arg Val Lys Val
2725 2730 2735

Gly Asp Cys Lys Ser Glu Glu Glu Val Asp Ile His Tyr Cys Glu Gly
2740 2745 2750

Lys Cys Ala Ser Lys Ala Val Tyr Ser Ile His Met Glu Asp Val Gln
2755 2760 2765

Asp Gln Cys Ser Cys Cys Ser Pro Thr Gln Thr Glu Pro Met Gln Val
2770 2775 2780

Ala Leu Arg Cys Thr Asn Gly Ser Leu Ile Tyr His Glu Ile Leu Asn
2785 2790 2795 2800

Ala Ile Glu Cys Arg Cys Ser Pro Arg Lys Cys Ser Lys
2805 2810

WE CLAIM:

1. An isolated nucleic acid comprising a nucleotide sequence encoding canine von Willebrand Factor polypeptide.

2. The isolated nucleic acid of Claim 1, wherein the nucleotide sequence is capable of hybridizing under high stringency conditions to SEQ ID NO. 1.

3. The isolated nucleic acid of Claim 1, wherein the nucleotide sequence encodes the Scottish terrier von Willebrand Factor polypeptide.

4. The isolated nucleic acid of Claim 2, wherein the nucleotide sequence encodes the Scottish terrier von Willebrand Factor polypeptide.

5. A vector comprising the nucleic acid of Claim 1.

6. A vector comprising the nucleic acid of Claim 2.

7. A cell comprising the vector of Claim 5.

8. A cell comprising the vector of Claim 6.

9. An isolated nucleic acid comprising a nucleotide sequence encoding defective canine von Willebrand Factor polypeptide.

10. The isolated nucleic acid of Claim 9, wherein the nucleotide sequence is capable of hybridizing under high stringency conditions to the complement of SEQ ID NO. 1 having a base deletion at codon 88.

11. A vector comprising the nucleic acid of Claim 9.

12. A vector comprising the nucleic acid of Claim 10.

13. A cell comprising the vector of Claim 11.

14. A cell comprising the vector of Claim 12.

15. An isolated oligonucleotide sequence consisting of contiguous nucleic acids of the nucleotide sequence of SEQ ID NO. 1 and capable of specifically hybridizing with the canine von Willebrand Factor gene.

16. An isolated oligonucleotide sequence consisting of contiguous nucleic acids of the nucleotide sequence that is complementary to the sequence of SEQ ID NO. 1 and capable of specifically hybridizing with the canine von Willebrand Factor gene.

17. A method of detecting a canine von Willebrand Factor gene in a sample comprising the steps of:

a) contacting the sample with a oligonucleotide comprising contiguous nucleic acids of the nucleotide sequence of SEQ ID NO. 1 and capable of specifically hybridizing with the canine von Willebrand Factor gene, under conditions favorable for hybridization of the oligonucleotide to any complementary sequences of nucleic acid in the sample; and

b) detecting hybridization, thereby detecting a canine von Willebrand Factor gene.

18. The method of Claim 17, further comprising the step of:

c) quantifying hybridization of the oligonucleotide to complementary sequence.

19. The method of Claim 17, wherein in SEQ ID NO. 1 there is a base deletion at codon 88.

20. An assay kit for screening for a canine von Willebrand Factor gene comprising:

a) an oligonucleotide comprising contiguous nucleic acids of the nucleotide sequence of SEQ ID NO. 1 and capable of hybridizing with the canine von Willebrand Factor gene;

b) reagents for hybridization of the oligonucleotide to a complementary nucleic acid sequence; and

c) container means for a)-b).

21. A method of detecting a canine von Willebrand Factor gene in a sample comprising the steps of:

a) contacting the sample with an oligonucleotide comprising contiguous nucleic acids of the nucleotide sequence that is complementary to the sequence of SEQ ID NO. 1 and capable of specifically hybridizing to the complementary nucleotide sequence, under conditions favorable for hybridization of the oligonucleotide to any complementary sequences of nucleic acid in the sample; and

b) detecting hybridization, thereby detecting a canine von Willebrand Factor gene.

22. The method of Claim 21, further comprising the step of:

c) quantifying hybridization of the oligonucleotide to complementary sequences.

23. The method of Claim 21, wherein in SEQ ID NO. 1 there is a base deletion at codon 88.

24. An assay kit for screening for a canine von Willebrand Factor gene comprising:

a) an oligonucleotide comprising contiguous acids from the nucleotide sequence that is complementary to the sequence of SEQ ID NO. 1 and capable of specifically hybridizing to the complementary nucleotide sequence;

b) reagents for hybridization of the oligonucleotide to a complementary nucleic acid sequence; and

c) container means for a)-b).

25. The assay kit of Claim 24, wherein in SEQ ID NO. 1 there is a base deletion at codon 88.

26. A method for detecting a mutated canine von Willebrand Factor gene in a canine DNA sample comprising the steps of:

a) amplifying the DNA sample by polymerase chain reaction to produce polymerase chain reaction products, wherein the polymerase chain reaction uses primers that produce a restriction site in a mutant allele but not in a normal allele;

b) digesting the polymerase chain reaction products with a restriction enzyme specific to the restriction site of the restriction site primer to produce DNA fragments; and

c) detecting the DNA fragments, thereby detecting a mutated canine von Willebrand Factor gene.

27. The method of Claim 26, wherein the primers are those of Figure 4.

28. The method of Claim 26, wherein the DNA fragments are detected by gel electrophoresis.

29. The method of Claim 27, wherein the restriction enzyme is *Bsi*EI.

30. The method of Claim 27, wherein the restriction enzyme is *Sau*96 I.

31. An oligonucleotide probe capable of detecting a mutation associated with canine von Willebrand's disease, wherein the mutation is a base deletion at codon 88 of the canine von Willebrand Factor gene.

FIGURE 1A

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   1 CATTAANAGG TCCTGGCTGG GAGCTTTTTT TTGGGACCAG CACTCCATGT TCAAGGGCAA
  61 ACAGGGGCCA ATTAGGATCA ATCTTTTTTC TTTCTTTTTT TAAAAAAAAA AATTCTTCCC
 121 ACTTTGCACA CGGACAGTAG TACATACCAG TAGCTCTCTG CGAGGACGGT GATCACTAAT
 181 CATTTCTCCT GCTTCGTGGC AGATGAGTCC TACCAGACTT GTGAGGGTGC TGCTGGCTCT
 241 GGCCCTCATC TTGCCAGGGA AACTTTGTAC AAAAGGGACT GTTGGAAGGT CATCGATGGC
 301 CCGATGTAGC CTTCTCGGAG GTGACTTCAT CAACACCTTT GATGAGAGCA TGTACAGCTT
 361 TGCGGGAGAT TGCAGTTACC TCCTGGCTGG GGACTGCCAG GAACACTCCA TCTCACTTAT
 421 CGGGGGTTTC CAAAATGACA AAAGAGTGAG CCTCTCCGTG TATCTCGGAG AATTTTTCGA
 481 CATTCATTTG TTTGTCAATG GTACCATGCT GCAGGGGACC CAAAGCATCT CCATGCCCTA
 541 CGCCTCCAAT GGGCTGTATC TAGAGGCCGA GGCTGGCTAC TACAAGCTGT CCAGTGAGGC
 601 CTACGGCTTT GTGGCCAGAA TTGATGGCAA TGGCAACTTT CAAGTCCTGC TGTCAGACAG
 661 ATACTTCAAC AAGACCTGTG GGCTGTGTGG CAACTTTAAT ATCTTTGCTG AGGATGACTT
 721 CAAGACTCAA GAAGGGACGT TGACTTCGGA CCCCTATGAC TTTGCCAACT CCTGGGCCCT
 781 GAGCAGTGGG GAACAACGGT GCAAACGGGT GTCCCCTCCC AGCAGCCCAT GCAATGTCTC
 841 CTCTGATGAA GTGCAGCAGG TCCTGTGGGA GCAGTGCCAG CTCCTGAAGA GTGCCTCGGT
 901 GTTTGCCCGC TGCCACCCGC TGGTGGACCC TGAGCCTTTT GTCGCCCTGT GTGAAAGGAC
 961 TCTGTGCACC TGTGTCCAGG GGATGGAGTG CCCTTGTGCG GTCCTCCTGG AGTACGCCCG
1021 GGCCTGTGCC CAGCAGGGGA TTGTCTTGTA CGGCTGGACC GACCACAGCG TCTGCCGACC
1081 AGCATGCCCT GCTGGCATGG AGTACAAGGA GTGCGTGTCC CCTTGCACCA GAACTTGCCA
1141 GAGCCTTCAT GTCAAAGAAG TGTGTCAGGA GCAATGTGTA GATGGCTGCA GCTGCCCCGA
1201 GGGCCAGCTC CTGGATGAAG GCCACTGCGT GGGAAGTGCT GAGTGTTCCT GTGTGCATGC
1261 TGGGCAACGG TACCCTCCGG GCGCCTCCCT CTTACAGGAC TGCCACACCT GCATTTGCCG
1321 AAATAGCCTG TGGATCTGCA GCAATGAAGA ATGCCCAGGC GAGTGTCTGG TCACAGGACA
1381 GTCCCACTTC AAGAGCTTCG ACAACAGGTA CTTCACCTTC AGTGGGGTCT GCCACTACCT
1441 GCTGGCCCAG GACTGCCAGG ACCACACATT CTCTGTTGTC ATAGAGACTG TCCAGTGTGC
1501 CGATGACCTG GATGCTGTCT GCACCCGCTC GGTCACCGTC CGCCTGCCTG GACATCACAA
1561 CAGCCTTGTG AAGCTGAAGA ATGGGGGAGG AGTCTCCATG GATGGCCAGG ATATCCAGAT
1621 TCCTCTCCTG CAAGGTGACC TCCGCATCCA GCACACCGTG ATGGCCTCCG TGCGCCTCAG
1681 CTACGGGGAG GACCTGCAGA TGGATTCGGA CGTCCGGGGC AGGCTACTGG TGACGCTGTA
1741 CCCCGCCTAC GCGGGGAAGA CGTGCGGCCG TGGCGGGAAC TACAACGGCA ACCGGGGGGA
1801 CGACTTCGTG ACGCCCGCAG GCCTGGCGGA GCCCCTGGTG GAGGACTTCG GGAACGCCTG
1861 GAAGCTGCTC GGGGCCTGCG AGAACCTGCA GAAGCAGCAC CGCGATCCCT GCAGCCTCAA
1921 CCCGCGCCAG GCCAGGTTTG CGGAGGAGGC GTGCGCGCTG CTGACGTCCT CGAAGTTCGA
1981 GCCCTGCCAC CGAGCGGTGG GTCCTCAGCC CTACGTGCAG AACTGCCTCT ACGACGTCTG
2041 CTCCTGCTCC GACGGCAGAG ACTGTCTTTG CAGCGCCGTG GCCAACTACG CCGCAGCCGT
2101 GGCCCGGAGG GGCGTGCACA TCGCGTGGCG GGAGCCGGGC TTCTGTGCGC TGAGCTGCCC
2161 CCAGGGCCAG GTGTACCTGC AGTGTGGGAC CCCCTGCAAC ATGACCTGTC TCTCCCTCTC
2221 TTACCCGGAG GAGGACTGCA ATGAGGTCTG CTTGGAAAGC TGCTTCTCCC CCCCAGGGCT
2281 GTACCTGGAT GAGAGGGGAG ATTGTGTGCC CAAGGCTCAG TGTCCCTGTT ACTATGATGG
2341 TGAGATCTTT CAGCCCGAAG ACATCTTCTC AGACCATCAC ACCATGTGCT ACTGTGAGGA
2401 TGGCTTCATG CACTGTACCA CAAGTGGAGG CCTGGGAAGC CTGCTGCCCA ACCCGGTGCT
2461 CAGCAGCCCC CGGTGTCACC GCAGCAAAAG GAGCCTGTCC TGTCGGCCCC CCATGGTCAA
2521 GTTGGTGTGT CCCGCTGATA ACCCGAGGGC TGAAGGACTG GAGTGTGCCA AAACCTGCCA
2581 GAACTATGAC CTGCAGTGCA TGAGCACAGG CTGTGTCTCC GGCTGCCTCT GCCCGCAGGG
2641 CATGGTCCGG CATGAAAACA GGTGTGTGGC GCTGGAAAGA TGTCCCTGCT TCCACCAAGG
2701 CCAAGAGTAC GCCCCAGGAG AAACCGTGAA AATTGACTGC AACACTTGTG TCTGTCGGGA
2761 CCGGAAGTGG ACCTGCACAG ACCATGTGTG TGATGCCACT TGCTCTGCCA TCGGCATGGC
2821 GCACTACCTC ACCTTCGACG GACTCAAGTA CCTGTTCCCT GGGGAGTGCC AGTATGTTCT
2881 GGTGCAGGAT TACTGCGGCA GTAACCCTGG GACCTTACGG ATCCTGGTGG GGAACGAGGG
2941 GTGCAGCTAC CCCTCAGTGA AATGCAAGAA GCGGGTCACC ATCCTGGTGG AAGGAGGAGA
3001 GATTGAACTG TTTGATGGGG AGGTGAATGT GAAGAAACCC ATGAAGGATG AGACTCACTT
3061 TGAGGTGGTA GAGTCTGGTC AGTACGTCAT TCTGCTGCTG GGCAAGGCAC TCTCTGTGGT
3121 CTGGGACCAC CGCCTGAGCA TCTCTGTGAC CCTGAAGCGG ACATACCAGG AGCAGGTGTG
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FIGURE 1B

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3181 TGGCCTGTGT GGGAATTTTG ATGGCATCCA GAACAATGAT TTCACCAGCA GCAGCCTCCA
3241 AATAGAAGAA GACCCTGTGG ACTTTGGGAA TTCCTGGAAA GTGAACCCGC AGTGTGCCGA
3301 CACCAAGAAA GTACCACTGG ACTCATCCCC TGCCGTCTGC CACAACAACA TCATGAAGCA
3361 GACGATGGTG GATTCCTCCT GCAGGATCCT CACCAGTGAT ATTTTCCAGG ACTGCAACAG
3421 GCTGGTGGAC CCTGAGCCAT TCCTGGACAT TTGCATCTAC GACACTTGCT CCTGTGAGTC
3481 CATTGGGGAC TGCACCTGCT TCTGTGACAC CATTGCTGCT TACGCCCACG TCTGTGCCCA
3541 GCATGGCAAG GTGGTAGCCT GGAGGACAGC CACATTCTGT CCCCAGAATT GCGAGGAGCG
3601 GAATCTCCAC GAGAATGGGT ATGAGTGTGA GTGGCGCTAT AACAGCTGTG CCCCTGCCTG
3661 TCCCATCACG TGCCAGCACC CCGAGCCACT GGCATGCCCT GTACAGTGTG TTGAAGGTTG
3721 CCATGCGCAC TGCCCTCCAG GGAAAATCCT GGATGAGCTT TTGCAGACCT GCATCGACCC
3781 TGAAGACTGT CCTGTGTGTG AGGTGGCTGG TCGTCGCTTG GCCCCAGGAA AGAAAATCAT
3841 CTTGAACCCC AGTGACCCTG AGCACTGCCA AATTTGTAAT TGTGATGGTG TCAACTTCAC
3901 CTGTAAGGCC TGCAGAGAAC CCGGAAGTGT TGTGGTGCCC CCCACAGATG GCCCCATTGG
3961 CTCTACCACC TCGTATGTGG AGGACACGTC GGAGCCGCCC CTCCATGACT TCCACTGCAG
4021 CAGGCTTCTG GACCTGGTTT TCCTGCTGGA TGGCTCCTCC AAGCTGTCTG AGGACGAGTT
4081 TGAAGTGCTG AAGGTCTTTG TGGTGGGTAT GATGGAGCAT CTGCACATCT CCCAGAAGCG
4141 GATCCGCGTG GCTGTGGTGG AGTACCACGA CGGCTCCCAC GCCTACATCG AGCTCAAGGA
4201 CCGGAAGCGA CCCTCAGAGC TGCGGCGCAT CACCAGCCAG GTGAAGTACG CGGGCAGCGA
4261 GGTGGCCTCC ACCAGTGAGG TCTTAAAGTA CACGCTGTTC CAGATCTTTG GCAAGATCGA
4321 CCGCCCGGAA GCGTCTCGCA TTGCCCTGCT CCTGATGGCC AGCCAGGAGC CCTCAAGGCT
4381 GGCCCGGAAT TTGGTCCGCT ATGTGCAGGG CCTGAAGAAG AAGAAAGTCA TTGTCATCCC
4441 TGTGGGCATC GGGCCCCACG CCAGCCTTAA GCAGATCCAC CTCATAGAGA AGCAGGCCCC
4501 TGAGAACAAG GCCTTTGTGT TCAGTGGTGT GGATGAGTTG GAGCAGCGAA GGGATGAGAT
4561 TATCAACTAC CTCTGTGACC TTGCCCCCGA AGCACCTGCC CCTACTCAGC ACCCCCCAAT
4621 GGCCCAGGTC ACGGTGGGTT CGGAGCTGTT GGGGGTTTCA TCTCCAGGAC CCAAAAGGAA
4681 CTCCATGGTC CTGGATGTGG TGTTTGTCCT GGAAGGGTCA GACAAAATTG GTGAGGCCAA
4741 CTTTAACAAA AGCAGGGAGT TCATGGAGGA GGTGATTCAG CGGATGGACG TGGGCCAGGA
4801 CAGGATCCAC GTCACAGTGC TGCAGTACTC GTACATGGTG ACCGTGGAGT ACACCTTCAG
4861 CGAGGCGCAG TCCAAGGGCG AGGTCCTACA GCAGGTGCGG GATATCCGAT ACCGGGGTGG
4921 CAACAGGACC AACACTGGAC TGGCCCTGCA ATACCTGTCC GAACACAGCT TCTCGGTCAG
4981 CCAGGGGGAC CGGGAGCAGG TACCTAACCT GGTCTACATG GTCACAGGAA ACCCCGCTTC
5041 TGATGAGATC AAGCGGATGC CTGGAGACAT CCAGGTGGTG CCCATCGGGG TGGGTCCACA
5101 TGCCAATGTG CAGGAGCTGG AGAAGATTGG CTGGCCCAAT GCCCCCATCC TCATCCATGA
5161 CTTTGAGATG CTCCCTCGAG AGGCTCCTGA TCTGGTGCTA CAGAGGTGCT GCTCTGGAGA
5221 GGGGCTGCAG ATCCCCACCC TCTCCCCCAC CCCAGATTGC AGCCAGCCCC TGGATGTGGT
5281 CCTCCTCCTG GATGGCTCTT CCAGCATTCC AGCTTCTTAC TTTGATGAAA TGAAGAGCTT
5341 CACCAAGGCT TTTATTTCAA GAGCTAATAT AGGGCCCCGG CTCACTCAAG TGTCGGTGCT
5401 GCAATATGGA AGCATCACCA CTATCGATGT GCCTTGGAAT GTAGCCTATG AGAAAGTCCA
5461 TTTACTGAGC CTTGTGGACC TCATGCAGCA GGAGGGAGGC CCCAGCGAAA TTGGGGATGC
5521 TTTGAGCTTT GCCGTGCGAT ATGTCACCTC AGAAGTCCAT GGTGCCAGGC CCGGAGCCTC
5581 GAAAGCGGTG GTTATCCTAG TCACAGATGT CTCCGTGGAT TCAGTGGATG CTGCAGCCGA
5641 GGCCGCCAGA TCCAACCGAG TGACAGTGTT CCCCATTGGA ATCGGGGATC GGTACAGTGA
5701 GGCCCAGCTG AGCAGCTTGG CAGGCCCAAA GGCTGGCTCC AATATGGTAA GGCTCCAGCG
5761 AATTGAAGAC CTCCCCACCG TGGCCACCCT GGGAAATTCC TTCTTCCACA AGCTGTGCTC
5821 TGGGTTTGAT AGAGTTTGCG TGGATGAGGA TGGGAATGAG AAGAGGCCCG GGGATGTCTG
5881 GACCTTGCCA GACCAGTGCC ACACAGTGAC TTGCCTGCCA GATGGCCAGA CCTTGCTGAA
5941 GAGTCATCGG GTCAACTGTG ACCGGGGGCC AAGGCCTTCG TGCCCCAATG GCCAGCCCCC
6001 TCTCAGGGTA GAGGAGACCT GTGGCTGCCG CTGGACCTGT CCCTGTGTGT GCATGGGCAG
6061 CTCTACCCGG CACATCGTGA CCTTTGATGG GCAGAATTTC AAGCTGACTG GCAGCTGTTC
6121 GTATGTCCTA TTTCAAAACA AGGAGCAGGA CCTGGAGGTG ATTCTCCAGA ATGGTGCCTG
6181 CAGCCCTGGG GCGAAGGAGA CCTGCATGAA ATCCATTGAG GTGAAGCATG ACGGCCTCTC
6241 AGTTGAGCTC CACAGTGACA TGCAGATGAC AGTGAATGGG AGACTAGTCT CCATCCCATA
6301 TGTGGGTGGA GACATGGAAG TCAATGTTTA TGGGACCATC ATGTATGAGG TCAGATTCAA
6361 CCATCTTGGC CACATCTTCA CATTCACCCC CCAAAACAAT GAGTTCCAGC TGCAGCTCAG
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FIGURE 1C

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6421 CCCCAGGACC TTTGCTTCGA AGACATATGG TCTCTGTGGG ATCTGTGATG AGAACGGAGC
6481 CAATGACTTC ATTCTGAGGG ATGGGACAGT CACCACAGAC TGGAAGGCAC TCATCCAGGA
6541 ATGGACCGTA CAGCAGCTTG GGAAGACATC CCAGCCTGTC CATGAGGAGC AGTGTCCTGT
6601 CTCCGAATTC TTCCACTGCC AGGTCCTCCT CTCAGAATTG TTTGCCGAGT GCCACAAGGT
6661 CCTCGCTCCA GCCACCTTTT ATGCCATGTG CCAGCCCGAC AGTTGCCACC CGAAGAAAGT
6721 GTGTGAGGCG ATTGCCTTGT ATGCCCACCT CTGTCGGACC AAAGGGGTCT GTGTGGACTG
6781 GAGGAGGGCC AATTTCTGTG CTATGTCATG TCCACCATCC CTGGTGTACA ACCACTGTGA
6841 GCATGGCTGC CCTCGGCTCT GTGAAGGCAA TACAAGCTCC TGTGGGGACC AACCCTCGGA
6901 AGGCTGCTTC TGCCCCCCAA ACCAAGTCAT GCTGGAAGGT AGCTGTGTCC CCGAGGAGGC
6961 CTGTACCCAG TGCATCAGCG AGGATGGAGT CCGGCACCAG TTCCTGGAAA CCTGGGTCCC
7021 AGCCCACCAG CCTTGCCAGA TCTGCACGTG CCTCAGTGGG CGGAAGGTCA ACTGTACGTT
7081 GCAGCCCTGC CCCACAGCCA AAGCTCCCAC CTGTGGCCCG TGTGAAGTGG CCCGCCTCCG
7141 CCAGAACGCA GTGCAGTGCT GCCCGGAGTA CGAGTGTGTG TGTGACCTGG TGAGCTGTGA
7201 CCTGCCCCCG GTGCCTCCCT GCGAAGATGG CCTCCAGATG ACCCTGACCA ATCCTGGCGA
7261 GTGCAGACCC AACTTCACCT GTGCCTGCAG GAAGGATGAA TGCAGACGGG AGTCCCCGCC
7321 CTCTTGTCCC CCGCACCGGA CGCCGGCCCT TCGGAAGACT CAGTGCTGTG ATGAGTATGA
7381 GTGTGCATGC AACTGTGTCA ACTCCACGGT GAGCTGCCCG CTTGGGTACC TGGCCTCGGC
7441 TGTCACCAAC GACTGTGGCT GCACCACAAC AACCTGCTTC CCTGACAAGG TGTGTGTCCA
7501 CCGAGGCACC ATCTACCCTG TGGGCCAGTT CTGGGAGGAG GCCTGTGACG TGTGCACCTG
7561 CACGGACTTG GAGGACTCTG TGATGGGCCT GCGTGTGGCC CAGTGCTCCC AGAAGCCCTG
7621 TGAGGACAAC TGCCTGTCAG GCTTCACTTA TGTCCTTCAT GAAGGCGAGT GCTGTGGAAG
7681 GTGTCTGCCA TCTGCCTGTG AGGTGGTCAC TGGTTCACCA CGGGGCGACG CCCAGTCTCA
7741 CTGGAAGAAT GTTGGCTCTC ACTGGGCCTC CCCTGACAAC CCCTGCCTCA TCAATGAGTG
7801 TGTCCGAGTG AAGGAAGAGG TCTTTGTGCA ACAGAGGAAT GTCTCCTGCC CCCAGCTGAA
7861 TGTCCCCACC TGCCCCACGG GCTTCCAGCT GAGCTGTAAG ACCTCAGAGT GTTGTCCCAC
7921 CTGTCACTGC GAGCCCCTGG AGGCCTGCTT GCTCAATGGT ACCATCATTG GGCCGGGGAA
7981 AAGTCTGATG ATTGATGTGT GTACAACCTG CCGCTGCACC GTGCCGGTGG GAGTCATCTC
8041 TGGATTCAAG CTGGAGGGCA GGAAGACCAC CTGTGAGGCA TGCCCCCTGG GTTATAAGGA
8101 AGAGAAGAAC CAAGGTGAAT GCTGTGGGAG ATGTCTGCCT ATAGCTTGCA CCATTCAGCT
8161 AAGAGGAGGA CAGATCATGA CACTGAAGCG TGATGAGACT ATCCAGGATG GCTGTGACAG
8221 TCACTTCTGC AAGGTCAATG AAAGAGGAGA GTACATCTGG GAGAAGAGAG TCACGGGTTG
8281 CCCACCTTTC GATGAACACA AGTGTCTGGC TGAGGGAGGA AAAATCATGA AAATTCCAGG
8341 CACCTGCTGT GACACATGTG AGGAGCCAGA ATGCAAGGAT ATCATTGCCA AGCTGCAGCG
8401 TGTCAAAGTG GGAGACTGTA AGTCTGAAGA GGAAGTGGAC ATTCATTACT GTGAGGGTAA
8461 ATGTGCCAGC AAAGCCGTGT ACTCCATCCA CATGGAGGAT GTGCAGGACC AGTGCTCCTG
8521 CTGCTCGCCC ACCCAGACGG AGCCCATGCA GGTGGCCCTG CGCTGCACCA ATGGCTCCCT
8581 CATCTACCAT GAGATCCTCA ATGCCATCGA ATGCAGGTGT TCCCCCAGGA AGTGCAGCAA
8641 GTGAGGCCAC TGCCTGGATG CTACTGTCGC CTGCCTTACC CGACCTCACT GGACTGGCCA
8701 GAGTGCTGCT CAGTCCTCCT CAGTCCTCCT CCTGCTCTGC TCTTGTGCTT CCTGATCCCA
8761 CAATAAAGGT CAATCTTTCA CCTTGAAAAA AAAAAAAAAA AA
```

```
Human   MIPARFAGVLLALALILPGTLCAEGTRGRSSTARCSLFGSDFVNTFDGSMYSFAGYCSYL    60
Dog     -S-T-LVR-----------K--TK--V----M-----L-G--I----E-------D----

Human   LAGGCQKRSFSIIGDFQNGKRVSLSVYLGEFFDIHLFVNGTVTQGDQRVSMPYASKGLYL   120
Dog     ---D--EH-I-L--G---D---------------------ML--T-SI------N----

Human   ETEAGYYKLSGEAYGFVARIDGSGNFQVLLSDRYFNKTCGLCGNFNIFAEDDFMTQEGTL   180
Dog     -A--------S-----------N-----------------------------K------

Human   TSDPYDFANSWALSSGEQWCERASPPSSSCNISSGEMQKGLWEQCQLLKSTSVFARCHPL   240
Dog     -----------------R-K-V-----P--V--D-V-QV----------A---------

Human   VDPEPFVALCEKTLCECAGGLECACPALLEYARTCAQEGMVLYGWTDHSACSPVCPAGME   300
Dog     -----------R---T-VQ-M--P-AV------A---Q-I---------V-R-A------

Human   YRQCVSPCARTCQSLHINEMCQERCVDGCSCPEGQLLDEGLCVESTECPCVHSGKRYPPG   360
Dog     -KE-----T-------VK-V---Q----------------H--G-A--S---A-Q-----

Human   TSLSRDCNTCICRNSQWICSNEECPGECLVTGQSHFKSFDNRYFTFSGICQYLLARDCQD   420
Dog     A--LQ--H-------L------------------------------V-H----Q----

Human   HSFSIVIETVQCADDRDAVCTRSVTVRLPGLHNSLVKLKHGAGVAMDGQDVQLPLLKGDL   480
Dog     -T--V----------L--------------H--------N-G--S-----I-I---Q---

Human   RIQHTVTASVRLSYGEDLQMDWDGRGRLLVKLSPVYAGKTCGLCGNYNGNQGDDFLTPSG   540
Dog     ------M--------------S-V------T-Y-A-------RG------R----V--A-

Human   LAEPRVEDFGNAWKLHGDCQDLQKQHSDPCALNPRMTRFSEEACAVLTSPTFEACHRAVS   600
Dog     ----L----------L-A-EN-----R---S----QA--A-----L---SK--P-----G

Human   PLPYLRNCRYDVCSCSDGRECLCGALASYAAACAGRGVRVAWREPGRCELNCPKGQVYLQ   660
Dog     -Q--VQ--L----------D---S-V-N----V-R---HI------F-A-S--Q------

Human   CGTPCNLTCRSLSYPDEECNEACLEGCFCPPGLYMDERGDCVPKAQCPCYYDGEIFQPED   720
Dog     ------M--L-----E-D---V---S--S-----L-----------------------

Human   IFSDHHTMCYCEDGFMHCTMSGVPGSLLPDAVLSSPLSHRSKRSLSCRPPMVKLVCPADN   780
Dog     -------------------T--GL-----NP-----RC---------------------

Human   LRAEGLECTKTCQNYDLECMSMGCVSGCLCPPGMVRHENRCVALERCPCFHQGKEYAPGE   840
Dog     P-------A--------Q---T---------Q--------------------Q------

Human   TVKIGCNTCVCRDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGECQYVLVQDYCGS   900
Dog     ----D-----------T-----------A-------------------------------

Human   NPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESGR   960
Dog     ----L------E---Y---------------------------K--------------Q

Human   YIILLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVD  1020
Dog     -V-------------HR-----T--R----Q---------------F---S--I------

Human   FGNSWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRILTSDVFQDCNKLVDPEPY  1080
Dog     -------NP-----K---------V---------------------I-----R------F
```

FIGURE 2A

Human	LDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGKVVTWRTATLCPQSCEERNLRENGY	1140
Dog	--I--------------T--------------------A-----F---N------H----	
Human	ECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQTCVDPEDCPVCE	1200
Dog	-------------PI-----------------------------------I---------	
Human	VAGRRFASGKKVTLNPSDPEHCQICHCDVVNLTCEACQEPGGLVVPPTDAPVSPTTLYVE	1260
Dog	-----L-P---II------------N--G--F--K--R---SV------G-IGS--S---	
Human	DISEPPLHDFYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRISQKWVRVAVVE	1320
Dog	-T--------H---------------K---D------V---G---H-H----RI------	
Human	YHDGSHAYIGLKDRKRPSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRI	1380
Dog	---------E-------------T--------E----------------G----------	
Human	ALLLMASQEPQRMSRNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVL	1440
Dog	----------S-LA--L-----------------------S----H-------------F	
Human	SSVDELEQQRDEIVSYLCDLAPEAPPPTLPPHMAQVTVGPGLLGVSTLGPKRNSMVLDVA	1500
Dog	-G------R----IN----------A--QH-P-------SE-----SP-----------V	
Human	FVLEGSDKIGEADFNRSKEFMEEVIQRMDVGQDSIHVTVLQYSYMVTVEYPFSEAQSKGD	1560
Dog	------------N--K-R---------------R----------------T--------E	
Human	ILQRVREIRYQGGNRTNTGLALRYLSDHSFLVSQGDREQAPNLVYMVTGNPASDEIKRLP	1620
Dog	V--Q--D---R-----------Q---E---S--------V------------------M-	
Human	GDIQVVPIGVGPNANVQELERIGWPNAPILIQDFETLPREAPDLVLQRCCSGEGLQIPTL	1680
Dog	------------H-------K----------H---M------------------------	
Human	SPAPDCSQPLDVILLLDGSSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITT	1740
Dog	--T---------V--------I-----------T-----R--------------------	
Human	IDVPWNVVPEKAHLLSLVDVMQREGGPSQIGDALGFAVRYLTSEMHGARPGASKAVVILV	1800
Dog	-------AY--V-------L--Q-----E-----S-----V---V---------------	
Human	TDVSVDSVDAAADAARSNRVTVFPIGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDLPTM	1860
Dog	------------E------------------SE---SS----KAG--M-R---------V	
Human	VTLGNSFLHKLCSGFVRICMDEDGNEKRPGDVWTLPDQCHTVTCQPDGQTLLKTHRVNCD	1920
Dog	A------F-------D-V-V------------------------L--------S------	
Human	RGLRPSCPNSQSPVKVEETCGCRWTCPCVCTGSSTRHIVTFDGQNFKLTGSCSYVLFQNK	1980
Dog	--P------G-P-LR---------------M-----------------------------	
Human	EQDLEVILHNGACSPGARQGCMKSIEVKHSALSVELHSDMEVTVNGRLVSVPYVGGNMEV	2040
Dog	--------Q--------KET---------DG---------QM--------I-----D---	
Human	NVYGAIMHEVRFNHLGHIFTFTPQNNEFQLQLSPKTFASKTYGLCGICDENGANDFMLRD	2100
Dog	----T--Y--------------------------R---------------------I---	
Human	GTVTTDWKTLVQEWTVQRPGQTCQPILEEQCLVPDSSHCQVLLLPLFAECHKVLAPATFY	2160
Dog	--------A-I------QL-K-S--VH----P-SEFF------SE---------------	

FIGURE 2B

```
Human   AICQQDSCHQEQVCEVIASYAHLCRTNGVCVDWRTPDFCAMSCPPSLVYNHCEHGCPRHC   2220
Dog     -M--P----PKK---A--L-------K-------RAN---------------------L-

Human   DGNVSSCGDHPSEGCFCPPDKVMLEGSCVPEEACTQCIGEDGVQHQFLEAWVPDHQPCQI   2280
Dog     E--T-----Q---------NQ-----------------S----R-----T---A------

Human   CTCLSGRKVNCTTQPCPTAKAPTCGLCEVARLRQNADQCCPEYECVCDPVSCDLPPVPHC   2340
Dog     ------------L------------P----------V----------L----------P-

Human   ERGLQPTLTNPGECRPNFTCACRKEECKRVSPPSCPPHRLPTLRKTQCCDEYECACNCVN   2400
Dog     -D---M------------------D--R-E---------T-A------------------

Human   STVSCPLGYLASTATNDCGCTTTTCLPDKVCVHRSTIYPVGQFWEEGCDVCTCTDMEDAV   2460
Dog     ------------AV-----------F--------G-----------A--------L--S-

Human   MGLRVAQCSQKPCEDSCRSGFTYVLHEGECCGRCLPSACEVVTGSFRGDSQSSWKSVGSQ   2520
Dog     ---------------N-L-------------------------------A--H--N---H

Human   WASPENPCLINECVRVKEEVFIQQRNVSCPQLEVPVCPSGFQLSCKTSACCPSCRCERME   2580
Dog     ----D----------------V----------N--T--T---------E---T-H--PL-

Human   ACMLNGTVIGPGKTVMIDVCTTCRCMVQVGVISGFKLECRKTTCNPCPLGYKEENNTGEC   2640
Dog     --L----I-----SL----------T-P----------G-----EA--------K-Q---

Human   CGRCLPTACTIQLRGGQIMTLKRDETLQDGCDTHFCKVNERGEYFWEKRVTGCPPFDEHK   2700
Dog     ------I-------------------I-----S-----------I---------------

Human   CLAEGGKIMKIPGTCCDTCEEPECNDITARLQYVKVGSCKSEVEVDIHYCQGKCASKANY   2760
Dog     ------------------------K--I-K--R----D----E-------E-------V-

Human   SIDINDVQDQCSCCSPTRTEPMQVALHCTNGSVVYHEVLNAMECKCSPRKCSK          2813
Dog     --HME------------Q--------R-----LI---I---I--R--------
```

FIGURE 2C

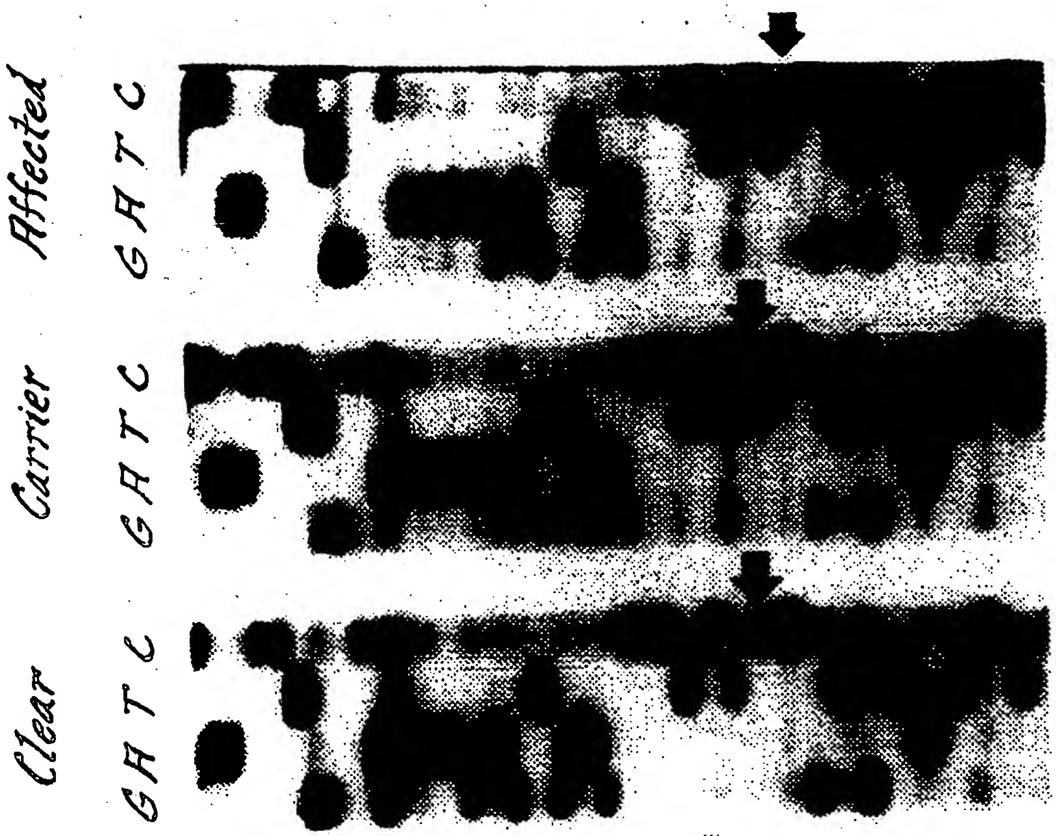

FIG. 7

```
exon 4        AAATGACAAAAGAGTGAGCCGGTC*
AGGGGGTTTCCAAAATGACAAAAGAGTGAGCCTCTCCGTGTATCTCGGAGAATTTTTCGA
  G  G  F  Q  N  D  K  R  V  S  L  S  V  Y  L  G  E  F  F  D

CATTCATTTGTTTGTCAATGGTACCATGCTGCAGGGGACCCAAAGGTAAGTCAGAAGCCC
  I  H  L  F  V  N  G  T  M  L  Q  G  T  Q  R

GAATGTTCAGGTTAATATGGACCCTGGGGATCACTTTGCAACCCCCTTGTTTTTTCAGAT

GAGGGAGCCGGGGCCCAGAGACAGGAAGTAAATGTGCCCAGGGAAAGTGAGTGGCAGGAC

TGGGTGAAAGCCCCATATCCCGACTCCTGGTCAAGGAGACTTTGCACCAAGGTCCCAGCC
                   3'-GGGCTGGCGACCAGTTCCTCTGAA-5'

CTGGAGCATGGGGTTGGGGTTGGAAGGTGGAGGGACATGGAGGAAATGCATGAGAAGCAC

                                        exon 5
GCTTCCTGAGCTCCTCCTTGTCCCACCAGCATCTCCATGCCCTACGCCTCCAATGGGC
                                       I  S  M  P  Y  A  S  N  G
```

FIGURE 4

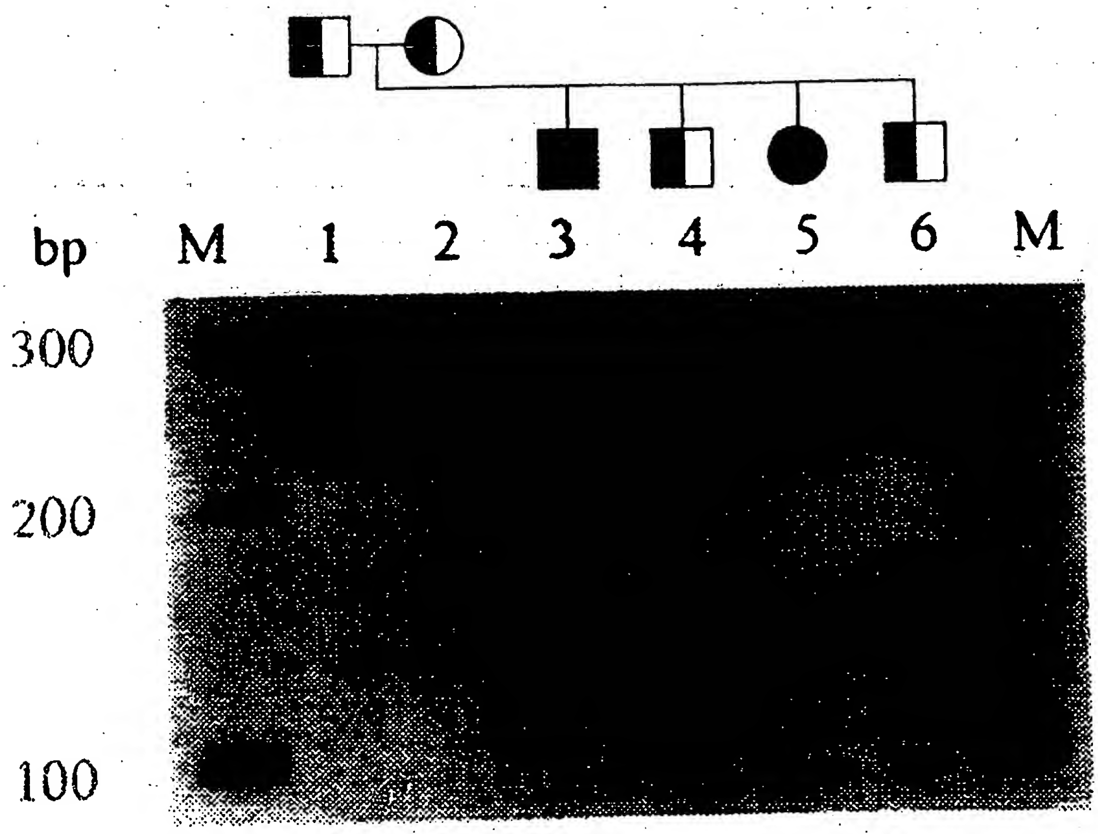

FIG. 5.

INTERNATIONAL SEARCH REPORT

International application No. PCT/US97/12606

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12Q 1/68; C12P 19/34; C07H 21/02, 21/04
US CL :435/6, 91.2; 536/23.1, 24.3, 24.33
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.2; 536/23.1, 24.3, 24.33

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y --- A	SHIBUYA, H. et al. A polymorphic $(AGGAAT)_n$ tandem repeat in an intron of the canine von Willebrand factor gene. Animal Genetics. April 1994, Volume 25, Number 2, page 122, see entire document.	15-22, 24-26, 28, 31 ------------ 1-14, 23, 27, 29

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
28 AUGUST 1997	14 NOV 1997

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	DIANNE REES Telephone No. (703) 308-0196

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, BIOSIS, BIOTECHABS, BIOTECHDS, CABA, DGENE, DRUGU, EMBASE, MEDLINE, EUROPATFULL, JAPIO, WPIDS, USPATFULL, GENBANK
search terms: von Willebrand, sequence, clone, cloning, probes, primers, hybridization, detection, nucleic acids,mutations, canine,dogs, Scottish terriers, primers in Figure 4.

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